Report

State of Oregon Department of Environmental Quality

PREDATOR: Development and use of RIVPACS-type macroinvertebrate models to assess the biotic condition of wadeable Oregon streams (November 2005 models)

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Rationale

The Oregon Department of Environmental Quality (DEQ) is responsible for protecting the waters of the state from pollution that may adversely affect drinking water, aquatic life and recreational uses. DEQ routinely monitors conventional water quality parameters such as nutrients, dissolved oxygen, pH, turbidity, conductivity and bacteria to report on the water quality status and trends in Oregon. However, resource limitations make it impractical to measure all the potential pollutants which may impair Oregon's waters. Aquatic insect communities are direct indicators of biological conditions and a surrogate for watershed health. They provide a cost effective screening tool for assessing and identifying problems that may require further examination.

The purpose of this document is to provide a background on predictive modelling, its utility, and the specific application of the macroinvertebrate models used by the Oregon DEQ.

What is a Predictive Model?

A predictive model, in this case, is a tool used to assess the integrity of an aquatic insect assemblage. Predictive modelling estimates the expected occurrence of macroinvertebrates at a sample location. This is done by developing a list of insect species that commonly occur at least disturbed, or reference, locations that have similar natural characteristic to the sample locations. The list of species generated from the reference locations is known as the "Expected" taxa list or "E". This list is compared to the captured aquatic insects or,"Observed" taxa ("O"), at an assessment site. The predictive model output is the observed to expected (O/E) taxa ratio. Scores less than one have fewer taxa at a site than were predicted by the model. Scores greater than one are either equivalent to the reference location or may have an enhanced insect community as a result of some type of enrichment.

Another way to think of the score is in terms of the percentage of taxa loss or gain. Values less than 1.0 represent a loss of common native reference taxa. Percent taxa loss or gain is defined as:

$$\mathbf{(O/E - 1.0) * 100}$$

A negative value means a sample has lost reference taxa, while a positive value means the sample has gained reference taxa

Why Macroinvertebrates?

Macroinvertebrates include freshwater insects, crustaceans, mollusks, bivalves and other invertebrates larger than one half millimeter in size. They are important because they occupy a central role in food chains and ecosystem processes (Wallace and Webster 1996). Macroinvertebrates are easy to collect, are relatively cheap to process and analyze, and show strong responses to many stressors. These benefits, make macroinvertebrates the most commonly used aquatic organisms for assessing stream biological integrity. For a thorough examination of the role of macroinvertebrates in assessing biological integrity, see Rosenberg and Resh (1993) and Wright et. al (2000).

The PREDictive Assessment Tool for Oregon (PREDATOR)

PREDATOR consists of three regional models that assess the biological integrity of wadeable streams across Oregon. DEQ developed the models to supply a scientifically rigorous bioassessment tool that is easy to apply and provides a more complete understanding of the stream conditions across Oregon.

Similar to other predictive models, PREDATOR, generates an expected occurrence probability (how likely a taxon is to occur) for each species at a test site. Common taxa at reference sites with similar environmental conditions will have higher occurrence probabilities at test sites. The sum of the occurrence probabilities is the expected number of reference taxa, "E". Expected taxa are restricted to those taxa that were found at reference sites used for building the model. In PREDATOR, only taxa with occurrence probabilities greater than 50% were used to calculate the expected taxa list (see Ostermiller and Hawkins 2004). The observed taxa, or "O", are the number of expected taxa that were actually collected at the test site.

The first predictive model of this kind, the River InVertebrate Prediction and Classification System (RIVPACS), was developed in Britain in the 1980's. Two excellent overviews of the RIVPACS approach to predictive modeling are the Western Center for Monitoring (2006) and the Centre for Ecology and Hydrology (2006). For a more detailed discussion of predictive models (and other bioassessment techniques), see Wright et al (2000).

How does a predictive model differ from a Multi-metric approach?

Another common method for assessing biological conditions is called the multi-metric approach. Unlike the predictive modeling approach which uses raw data, the multi-metric approach summarizes biological data into groups. These groups are based on knowledge about the life history of the assessment organisms and convey information about the conditions of the river or stream they live in. Biological metrics are often selected to provide information on different aspects of the stream conditions or species composition like temperature preferences, nutrient preferences, the percentage of alien species, functional feeding groups, etc. The metrics are analyzed to determine which ones are most sensitive to disturbance. Once the metrics are selected, they are added together to create single score called an Index of Biological Integrity, or IBI. The final score is an index value for making comparisons with reference sites and other locations. Unlike the predictive modeling approach it does not represent the loss or gain of taxa at a site.

DEQ uses a multi-metric method for assessing fish and aquatic vertebrate assemblages. In the past, DEQ used the multi-metric approach to assess macroinvertebrate assemblages in Oregon but these indexes were developed using smaller-scale datasets which limited their applicability to other areas of the state.

Developing the Models

There were five main steps to developing the PREDATOR models:

1) Establishing consistent macroinvertebrate sampling protocols and collection periods

2) Selecting regional reference sites
3) Grouping reference sites based on the macroinvertebrate communities
4) Relating reference groups to predictor variables
5) Assessing model performance

Macroinvertebrate Sampling Protocols

Macroinvertebrate data from three sources, Utah State University (USU), the Washington Department of Ecology (WDOE) and DEQ were used to develop PREDATOR. In order to use data from multiple sources, consistent sampling protocols were necessary. A consistent level of sampling effort is important for developing precise predictive models. While there were slight differences in sampling methods, all three sources collected with the same sampling effort. DEQ macroinvertebrate sampling followed the standard methods described in the DEQ Mode of Operations Manual (DEQ 2004).

Basic sampling methods included the following:

Sampling season:	Summer low flow (late June to early October)
Habitat:	fast water (riffle)
Sample location:	systematic random selection
Collection device:	D-frame kicknet, 500 µm mesh
Sample area:	
DEQ:	1998-2002 = 2 ft x 1 ft (4 composited kicks);
	2003-2004 = 1 ft x 1 ft (8 composited kicks)
USU:	1998-2004 = 1 ft x 1 ft (8 composited kicks)
WDOE:	1998-2004 = 2 ft x 1 ft (4 composited kicks)
Total area:	8-ft^2, one composite sample
Laboratory Sub-sample:	max. 500 individuals; 10x magnification
Identification:	typically genus/species; Chironomidae to sub-family/tribe

Taxonomy

Predicative models require a consistent level of taxonomy be applied to all samples used to build and assess the models (Moss et. al 1999, Ostermiller and Hawkins 2004). Some more highly resolved taxa were aggregated to a less resolved taxonomic category (e.g., all species in one genus were grouped together). Alternatively, some less resolved taxa were excluded from analyses and more highly resolved taxa were retained (e.g., specimens that were only able to be identified to family were deleted from datasets if the vast majority of individuals within that same family were able to be identified to the genus level). A hypothetical example of this procedure is shown below (Table 1). These exercises resulted in a list of operational taxonomic units (OTUs) that vary in their level of taxonomic resolution, but are unique from one another (no ambiguous taxa).

In the example presented in Table 1, the less resolved "Baetidae" were dropped from the analyses because there were few individuals identified to this level, plus there were many individuals identified to more highly resolved (genus and species) levels. In contrast, all the species level identifications under the genera "*Baetis*" were aggregated up to the genus level. Again, in this case more information (individuals) was available at the genus level than at the species level. Also, note that "*Diphetor hageni*" is at the species level, while the other two taxa ("*Baetis*" and "*Acentrella*") were kept at the genus level. This is acceptable, as long as each taxon is unique from all other taxa.

Table 1. A hypothetical example of how consistent taxonomic levels are achieved. ("Lowest level identification" = the lowest taxonomic level achieved by an expert taxonomist. "Sample abundance" = the number of individuals collected at a site. "Unique taxa" = a taxonomic level where there are no individuals in a sample at a lower, related taxonomic level.)

Site name	Lowest level identification	Taxonomic level	Sample Abundance	Unique Taxa	Action	Operational Taxonomic Units	Model abundance
Fox Creek	Baetidae	Family	7	No	Exclude	--	--
Fox Creek	*Baetis*	Genus	132	No	None	*Baetis*	150
Fox Creek	*Baetis tricaudatus*	Species	13	Yes	Aggregate to genus	*Baetis*	--
Fox Creek	*Baetis bicaudatus*	Species	2	Yes	Aggregate to genus	*Baetis*	--
Fox Creek	*Baetis alius*	Species	3	Yes	Aggregate to genus	*Baetis*	--
Fox Creek	*Acentrella*	Genus	15	Yes	None	*Acentrella*	15
Fox Creek	*Diphetor hageni*	Species	4	Yes	None	*Diphetor hageni*	4

A table of OTUs and phylogenetic classification for the November 2005 PREDATOR models is shown in Appendix A. The full table is available for download from the Western Center for Monitoring (2006). Future versions of PREDATOR are likely to have differing levels of taxonomy for certain groups (e.g., chironomidae) than the current models. Our objectives will always be to increase taxonomic information as much as possible, while maintaining high model performance. Each subsequent version of PREDATOR will include full documentation of OTU levels.

The goal of assigning OTUs is to retain as much taxonomic information as possible. Optimally, all taxa in a sample would be identified to species, accounting for differing ecological requirements. However, the taxonomic literature allows for only certain groups of taxa to be identified to species. Additionally, some laboratories routinely identify certain groups of taxa to less resolved levels than others, limiting the taxonomic level to which those groups can be pooled across labs. For instance, in the PREDATOR models we combined data from three separate taxonomic laboratories. The trichoptera genus *Rhyacophila* was identified to species group for two of these laboratories, but to the less resolved genus for the third laboratory (47% of reference samples, and most of the eastern Oregon reference samples). There do appear to be differing ecological requirements among the species groups which could be useful in the models, but using the species group as the OTU for this set of taxa would have resulted in throwing out all individuals identified to the genus level. This would mean that all information related to

Rhyacophila would be discarded for ~47% of the reference sites used in development of RIVPACS models. The real question then becomes: Is the information at the genus level of *Rhyacophila* more important to retain for all reference sites? Or are the species groups so different in their ecological requirements that it makes more sense to have no information for this group at 47% of reference sites. Local experts and DEQ databases of ecological traits were consulted when ultimately making decisions on whether to aggregate or discard taxa from the models.

Next, the 500 organism count from each sample is randomly sub-sampled to 300 individuals using a simple computer routine. Model precision and accuracy was shown to increase with sub-sampled counts up to ~300 individuals (Ostermiller and Hawkins 2004). The purpose of this sub-sampling routine is to standardize the effort across samples. Species richness metrics such as O/E are highly correlated to the total amount of sample sorted, thus samples with more individuals have a greater likelihood of having higher O/E scores. By standardizing the sub-sample count to 300, we are attempting to even out the effects of differing sample sizes. Reference samples that contained less than 200 OTU individuals were excluded from the model building process. Samples may not have had at least 300 individuals due to either low productivity (naturally low in macroinvertebrate abundance) or many individuals were dropped because they were not identified to the appropriate taxonomic level (OTU). The "subsample.exe" program is available for download at the WCM website (Western Center for Monitoring 2006).

Macroinvertebrate assemblages were sampled during the summer months (June through early October) from 1998-2004. Sample sites included a wide range of wadeable stream types and span nearly all of the major ecoregions in the State of Oregon. Sites were surveyed either as part of random probabilistic surveys or as hand-picked reference sites using best professional judgment. During field collection, sites were also screened for approximately 30 human activities at the reach scale. Those activities closer to the stream bank were assigned higher scores. Post-sampling, all sites were screened based on the degree of human activities in their drainage areas for road density, urban and agricultural use, and active or recent logging (Drake 2004). A total of 205 reference sites were chosen for model calibration; 125 of the sites were sampled by DEQ, 96 were sampled by Utah State University (USU), and 6 were sampled by Washington Department of Ecology (WDOE). We included sites from Washington State to allow for assessment of conditions in the Columbia Plateau ecoregion, where DEQ has not currently identified any reference sites. For a thorough discussion of the reference condition approach, see Reynoldson et. al 1997 and Stoddard et. al 2006.

Model Development

Reference sites were grouped according to the similarities of their sampled invertebrate assemblages. This was accomplished through *cluster analysis*, and is based entirely on the biology. Clustering was performed using the Sorenson dissimilarity distance measure and flexible beta linkage ($\beta = -0.6$) (McCune and Grace 2002, Van Sickle et. al 2006). The choice of beta level was made to reduce the amount of chaining in the resulting dendrogram and to aid in the identification of reference groups. Reference groups were identified by "pruning" the resulting dendrogram at a level that maximized with-in group fidelity, as well as group size ($\geq$ 5 sites). All groups were formed by pruning across the dendrogram at the same height.

The resulting reference groups were then evaluated against numerous environmental variables to determine what non-anthropogenic factors best predicted reference group membership. These environmental variables and associated reference site groups create the basis for predictive models. With a predictive model a test site is assigned a likelihood of belonging to each reference group, based on the values of environmental (predictor) variables. The set of predictor variables that best explained differences in reference groups was determined through *discriminant function analysis (DFA)* (McCune and Grace 2002). All possible combinations of predictor variables (best-subsets) were screened (Van Sickle et al. 2006). Other statistical methods for predicting group membership, such as Classification and Regression Tree or Random Forests, were not explored. These methods offer promise in improving our attempts to model the environmental drivers of biological reference groups, but at the time we developed these models the literature in relation to stream bioassessment was sparse (Cao et. al 2007).

Only variables that are unlikely to be affected by human disturbance were used to determine the probability of a test site belonging to each reference group. Human disturbances can alter certain habitat or chemical variables, which can result in inaccurate predictions. (For example: Say a model uses conductivity as the only predictor variable and some reference groups have naturally low conductivity, while other reference groups have naturally high conductivity. If a test site we wish to assess with the model is in a stream with naturally low conductivity, but is immediately downstream of an irrigation return flow—which in this case artificially raises the conductivity—the model would inappropriately predict bugs at the test site similar to those bugs found at high conductivity reference sites.)

We examined a variety of predictor variables to see which ones best predicted the biological groups of the reference sites (Appendix B). We limited the variables to those that could be obtained from GIS coverages to minimize the amount of time and effort in the field. All that is required from a field crew is a macroinvertebrate sample and an accurate latitude and longitude. All other predictor information can be obtained in an office setting.

For a more detailed description of predictive modeling, as well as many literature resources, see the WCM website (Western Center for Monitoring 2006).

Null Models

In some cases, it may not be advantageous to develop a predictive model. This can occur for a variety of reasons, such as too few reference sites or environmental variables that do not allow for more accurate predictions. A null model is an alternate approach that is not based on a prediction of reference taxa using multivariate statistics. A null model does not use any clustering of reference sites into groups. The expected taxa list (E) is the common reference taxa—those taxa that occur at greater than 50% of the reference sites used in the null model. “O” then is the taxa that were expected and collected at a site (the taxa that count towards O are limited to those that were included in E). Besides offering an assessment option when predictive modeling does not work, null models also provide a comparison to see how much precision and accuracy we gain through predictive modeling process. If our predictive models do not show a significant level of improvement in model precision and accuracy, it is hard to justify the additional work required to make and use the predictive models.

Scoring a test sample using the null model is simple. The expected number of reference taxa (E) is always the same, because there is no predictive function. “E” is simply the sum of the frequency of occurrences of the ten taxa collected in 50% or more of the reference sites (Table 2). For the PREDATOR—NBR null model, E is always equal to 7.6. “O” then is the sum of how many of the ten reference taxa were observed in the sample.

Final Model Selection

The scale at which models are developed and applied affects their accuracy and precision. Based on the number and location of reference sites in Oregon, we examined several approaches: 1) a single statewide model, 2) separate Eastern and Western Oregon models, and 3) Level II ecoregions. A single Oregon model covering the entire state lacked adequate precision. The standard deviation (SD) of reference site O/E scores in our statewide model was never less than 0.20. A SD ~ 0.17 is generally viewed as an acceptable target (Western Center for Monitoring 2006). Next we attempted to split the state into two regions, “East” and “West”, with the Cascades crest as the division. Model results were unsatisfactory compared with previous modeling attempts within Oregon, so we proceeded to examining smaller regional models. It was not possible to create level III ecoregion models due to the small sample sizes of reference sites in all but a few ecoregions, nor was it possible to create models based on river basins. Our best regional models approximated level II ecoregions. Models at this scale maximized both sample size and inclusion of as much of the state as possible. In the end, two predictive models and one null model were developed for Oregon (Table 2, Figure 1). (See Appendix C for a list of reference sites and environmental data used in each model.) The Marine Western Coastal Forest (MWCF) predictive model covers streams in the Coast Range and Willamette Valley ecoregions. The Western Cordillera + Columbia Plateau (WC+CP) predictive model covers streams in the Klamath Mountains, Cascades, East Cascades, Blue Mountains, and Columbia Plateau ecoregions. The Northern Basin and Range (NBR) null model covers streams in southeastern Oregon.

There are a few things to note about these models. First, the southeastern part of Oregon (Northern Basin and Range level III ecoregion) is assessed using a null model. We found that including these nine reference sites in any of our other predictive models significantly reduced model performance. Including samples from this region in any of our other models always resulted in reduced model performance. Second, the types of streams used to build the models were wadeable (typically first- through fourth-order) streams that contained fast water habitats (riffles). Third, the Columbia Plateau is not actually a part of the Western Cordillera level II ecoregion. It is a part of the same level II ecoregion (Western Interior Basin and Ranges) as the southeastern Oregon sites used in the null model. However, we found that including the Columbia Plateau reference sites with the reference sites from the Western Cordillera level II ecoregion did not reduce predictive model performance.

These three models cover all level III ecoregions in Oregon, except for the Snake River Plains in far eastern Oregon (Figure 1). Currently, DEQ does not have any reference sites in this ecoregion. In the future, we plan to utilize reference sites in this ecoregion identified by the Idaho Department of Environmental Quality, as we did in the Columbia Plateau by using reference sites from Washington.

Table 2. PREDATOR model specifications for three regions in Oregon. (See Appendix A for variable descriptions.)

	Marine Western Coastal Forest (MWCF)	Western Cordillera + Columbia Plateau (WC+CP)	Northern Basin and Range (NBR)
Type of Model	Predictive	Predictive	Null
Regions	Level 2 ecoregion: Coast Range & Willamette Valley	Level 2 ecoregion + : Cascades, Klamath Mountains, East Cascades, Blue Mountains, + Columbia Plateau	Level 3 ecoregion: Northern Basin and Range
Stream type	Wadeable, fast water	Wadeable, fast water	Wadeable, fast water
Predictor variables	Julian date, longitude	Eastern Oregon, elevation, mean annual precipitation, annual maximum air temperature	None
Reference groups	3	5	1
Temporal range	1998-2004	1998-2004	1999-2004
Occurrence Probability (probability of capture	0.5	0.5	0.5
Organism sample count #	300	300	300
Minimum # of organisms	200	200	200
# of reference sites	38	167	9
Null model taxa	n/a	n/a	*Baetis*, Chironominae, *Optioservus*, Orthocladiinae, *Rhyacophila*, Trombidiformes, *Diphetor_hageni, Epeorus, Zaitzevia, Brachycentrus*

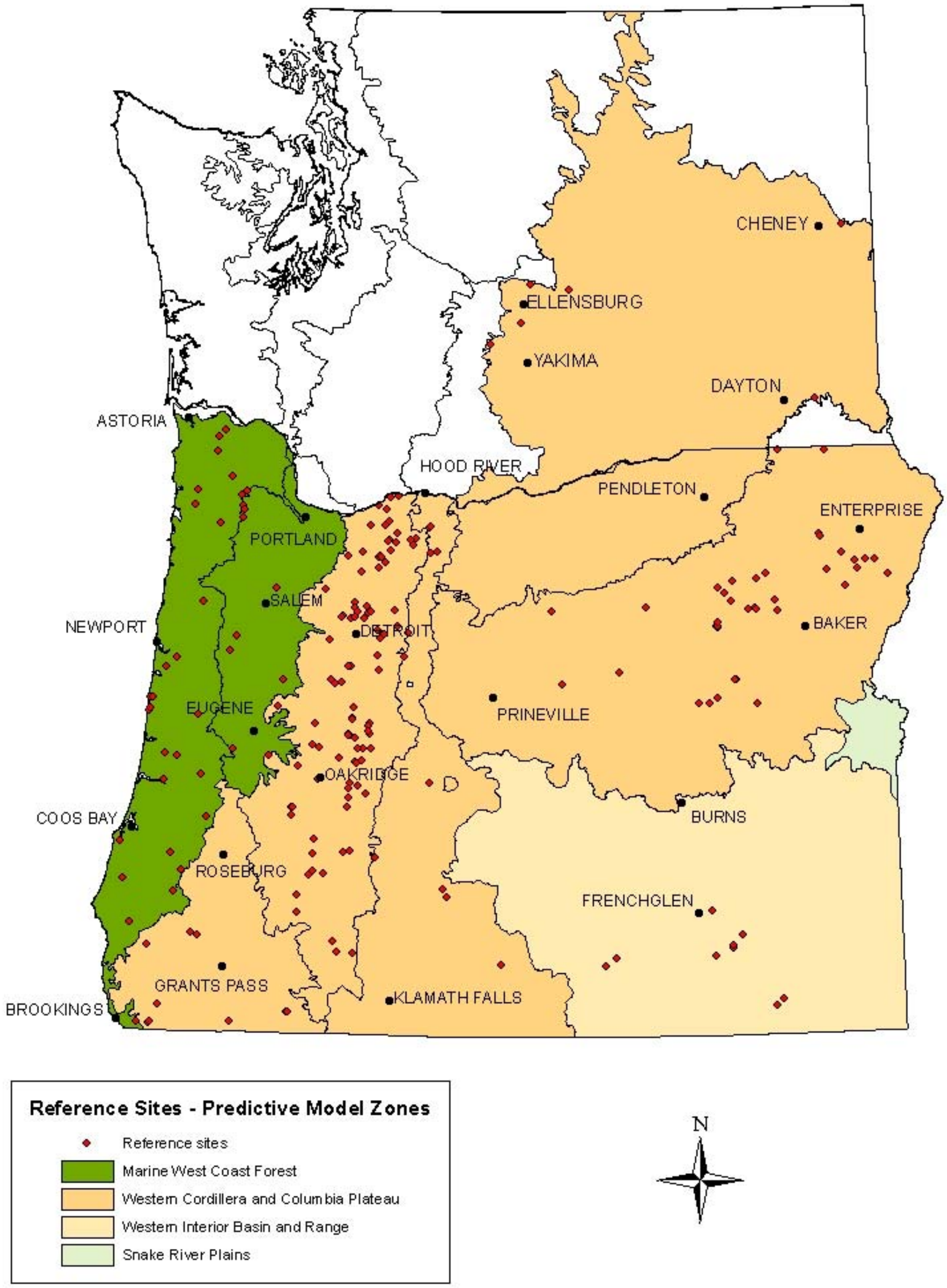


Figure 1. PREDATOR consists of two predictive models (1-Marine West Coast Forest, 2-Western Cordillera and Columbia Plateau) and one null model (Western Interior Basin and Range). No model exists for the Snake River Plains ecoregion.

Assessing model quality

This section is provided for those interested in how DEQ assessed model accuracy and precision. More detailed information about measuring model performance can be found at the WCM website (Western Center for Monitoring 2006), Ostermiller and Hawkins (2004), and Van Sickle et. al (2005).

Statistical results of the three final models are shown in Table 3. The MWCF and WC+CP models showed substantial improvement over the null models for each region. The "Null model" represents the upper end of variability that our models try to improve upon. If a predictive model does not show significant reductions in model errors over a null model, then it does not make sense to make a more complicated model. "Replicate sampling error" represents the lowest amount of variability we can expect to achieve in our models. A good model will show results closer to the replicate sampling error than to the null model error. For a more thorough examination of the use of null model errors and replicate sampling errors as upper and lower baselines for model performance, see Van Sickle et al. (2005).

Accuracy and precision can be examined in several ways (Western Center for Monitoring 2006). One way to estimate model accuracy is to look at the mean O/E scores of the sites used to build the models. Accurate models have a mean O/E close to 1.0. All three of our models' mean O/E values (for the reference sites used to build the models) are essentially 1.0 (Table3). Another way to examine model accuracy is to examine a plot of "O" versus "E" for the reference sites used to build the model. An accurate model should have a scatterplot that resembles a 1:1 line (i.e., a regression line slope close to 1.0 and an intercept close to 1.0). The slope of the regression lines for the MWCF model was 1.2 and the slope of the WC+CP model was 1.1 (Figure 2). Both models approximate the 1:1 line well.

Model precision can be estimated in two ways. One is to examine the spread of O/E scores in reference sites, represented by the standard deviation of O/E values. Precise models typically result in predictive model standard deviations of approximately 0.15 (Western Center for Monitoring 2006). The MWCF model was very precise with a predictive model standard deviation of 0.12, while the WC+CP model showed good precision with a model standard deviation of 0.15 (Table 3). Another way to examine precision is to look at the amount of variation in "O" that is predicted by "E", which is represented by the r^2 value from a regression of "O" to "E" at reference sites (Figure 2). In general, good models have r^2 values between 0.5-0.75. The MWCF r^2 (0.66) showed good precision, while the WC+CP r^2 (0.33) suggests lower precision for this model.

Comparisons to other PNW RIVPACS-type models

The predictive models developed for Oregon compare favorably to other RIVPACS-type models developed in the Pacific Northwest (PNW). Precision (measured as SD) of the WC+CP predictive model was similar to models created from Wyoming (Hargett et. al 2007) and all of Oregon (Van Sickle et. al 2006). The precision of the MWCF model was similar to a model for Western Oregon and Washington (Ostermiller and Hawkins 2004). For all of the PNW models, candidate predictor variables were fairly similar.

Sampling date, spatial location, stream size and power, geology, ecoregions, and climate variables were common to all modeling exercises. In all of these models, the trend seems to be to try to utilize predictor variables than can be derived through geographical information systems (GIS) exercises, rather than collecting more intensive field data. The number of final predictor variables used in the MWCF and WC+CP were lower than in Hargett et. al (2007) and Ostermiller and Hawkins (2004). In our models, we followed the results of Van Sickle et. al (2006) and used lower order (number of final variables) models in an attempt to avoid overfitting.

Table 3. PREDATOR 2005 model performance statistics. Model performance is shown for reference sites in level III ecoregions used to build the respective predictive models. "n" = sample size, "O/E" = observed/expected, and "SD" = standard deviation of O/E scores.

Model	N	Mean O/E	SD
Marine Western Coastal Forest	**38**		
Null model		1.00	0.14
Predictive model		0.99	0.12
Replicate sampling error			0.11
Coast Range	28	0.98	0.12
Willamette Valley	10	1.04	0.14
Western Cordillera + Columbia Plateau	**167**		
Null model		1.00	0.18
Predictive model		1.01	0.15
Replicate sampling error			0.13
Cascades	101	1.01	0.17
East Cascades	11	0.97	0.17
Klamath Mountains	10	0.99	0.13
Blue Mountains	39	1.02	0.12
Columbia Plateau	6	1.12	0.10
Northern Basin and Range	**9**		
Null model		1.00	0.29

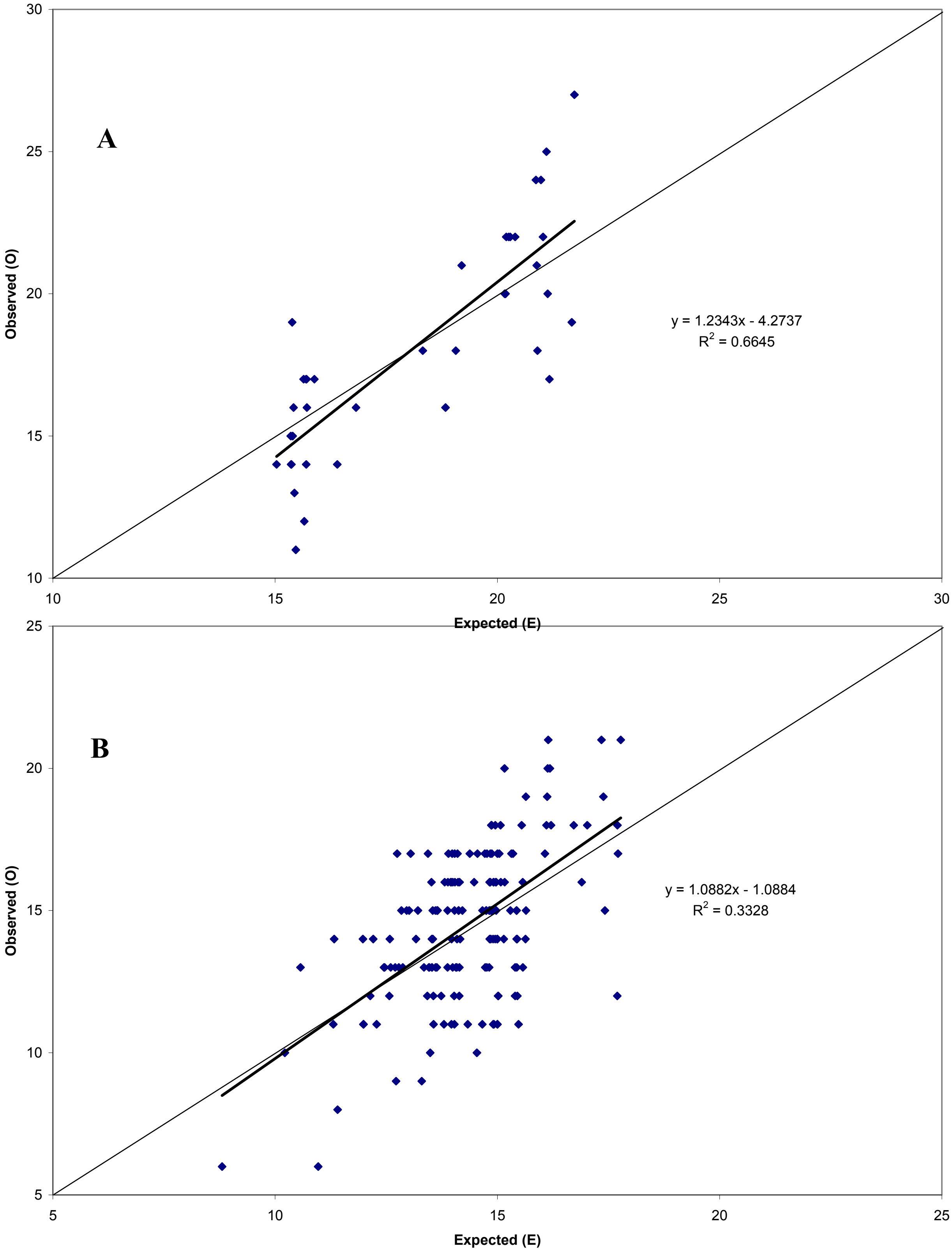


Figure 2. Performance of the MWCF model (panel A) and of the WC+CP model (panel B). The solid line is the 1:1 line representing a perfect relationship between Observed (O) and Expected (E). The dashed line is the regression line between O and E. The r^2 represents the percent of O explained by E.

In theory, the predictor variables used in development of RIVPACS models should be unaffected by anthropogenic disturbances. However, in practice, this is not always followed. Harget et. al (2007) and Ostermiller and Hawkins (2004) used substrate composition metrics as predictor variables, and they were also used in the original RIVPACS models developed in Britain (Wright et. al 1984). Increased human activities in a watershed are routinely linked to increases in fine sediments. Thus, predictions based on sediment composition may come at risk of introducing unquantifiable bias towards disturbed conditions. Our models performed comparably to other predictive models in the region, while maintaining "purity" of predictor variables.

Null model performance

Performance of the Northern Basin and Range (NBR) null model cannot be assessed in the same way as predictive models. By definition, the mean O/E value for the reference sites used to build the null model is 1.0 (Table 3). Precision can be estimated by looking at the SD of O/E values for reference sites (Table 3). The high SD of O/E values for reference sites suggests low precision. Obviously, having only nine reference sites in the NBR limits our confidence in our assessment of biological condition in this region.

Using the models

A separate report is available on the Xerces Society website (http://www.xerces.org/aquatic/predator/) which outlines in detail the data formatting requirements for the bug and predictor variables data files. It is crucial to follow the details of this report closely, as the software on the WCM website has very specific requirements.

PREDATOR outputs

When a user submits properly formatted predictive model files to the WCM website, the predictive model software generates four output files. For a basic analysis we are primarily concerned with two files: "Site Test Results" and "O Over E". Both the "Probability Matrix" and "Summary" files are useful for determining why a site may be disturbed (see Western Center for Monitoring 2006). (See below for further descriptions on how to use these outputs.)

Site Test Results--This file shows if a sample was within the experience of the model. This means that the predictor variables at a test site were within the range of the predictor variables at reference sites used to build the model. A chi-squared test is used to declare outliers based on the multivariate distance between a site's set of predictor values, and the values seen at reference sites. Samples outside of the experience of the reference sites used to build the model are considered outliers and are flagged as such in the "Site Test Results" file. They will still be scored, but it is up to the user to determine if the assessment is valid. It is important to note that this test is for predictor variables only.

Other important variables, such as year or sample abundances are not included (see the next paragraph).

An example of the potential pitfalls of assessing outlier samples that are not identified in the "Site Test Results" file is shown in Figure 3. O/E scores are shown for four groups of samples assessed by the MWCF model. "Count Outlier" samples had less than 200 individual macroinvertebrates and "Year Outlier" samples were collected in years earlier than the reference sites used to build the MWCF model. All "Test" sites were within the model bounds of bug count and sample year. Mean O/E scores from both count outlier (0.77) and year outlier (0.86) populations are lower than the mean O/E scores for the test population (0.91). Low counts (<200 bugs) affected O/E scores more than assessing a sample collected prior to 1998. This is not surprising, since fewer bugs in a sample should reduce the likelihood of collecting the expected taxa. Similarly, the bias towards lower O/E scores in year outlier samples could also be due to low numbers of macroinvertebrates. One of the major methods changes in macroinvertebrate sampling, beginning in 1999, was to increase the sub-sampling effort from 300 to 500 individuals.

To assess how PREDATOR models score data collected beyond timeframe the initial model development (post 2004), DEQ should continue to re-sample reference sites to track model scores. If reference sites used to build the model show O/E scores deviating from 1.0, then it may be necessary to re-calibrate the model with more current data.

Figure 3 illustrates the need to assess samples outside of the model experience with caution. The "Site Test Results" file will notify the user if the predictor variables for a test sample are beyond the experience of the model. However, it is the users' responsibility to ensure their samples are in the correct regions, were sampled in the correct season, follow similar collection and processing protocols, have enough bugs, and were sampled no earlier than 1998. Failure to comply with any one of these conditions may lead to inaccurate predictions of O/E.

O Over E--This file contains model scores (O/E), as well as the number of observed reference taxa (O), and the number of expected reference taxa (E). The output includes calculations for two probability of capture (P_c) thresholds: 0 and 0.5. The PREDATOR models are based on $P_c > 0.5$ (this means the model uses only bugs with a greater than 50% likelihood of being collected at reference sites). Make sure you use the O/E scores associated with $P_c > 0.5$.

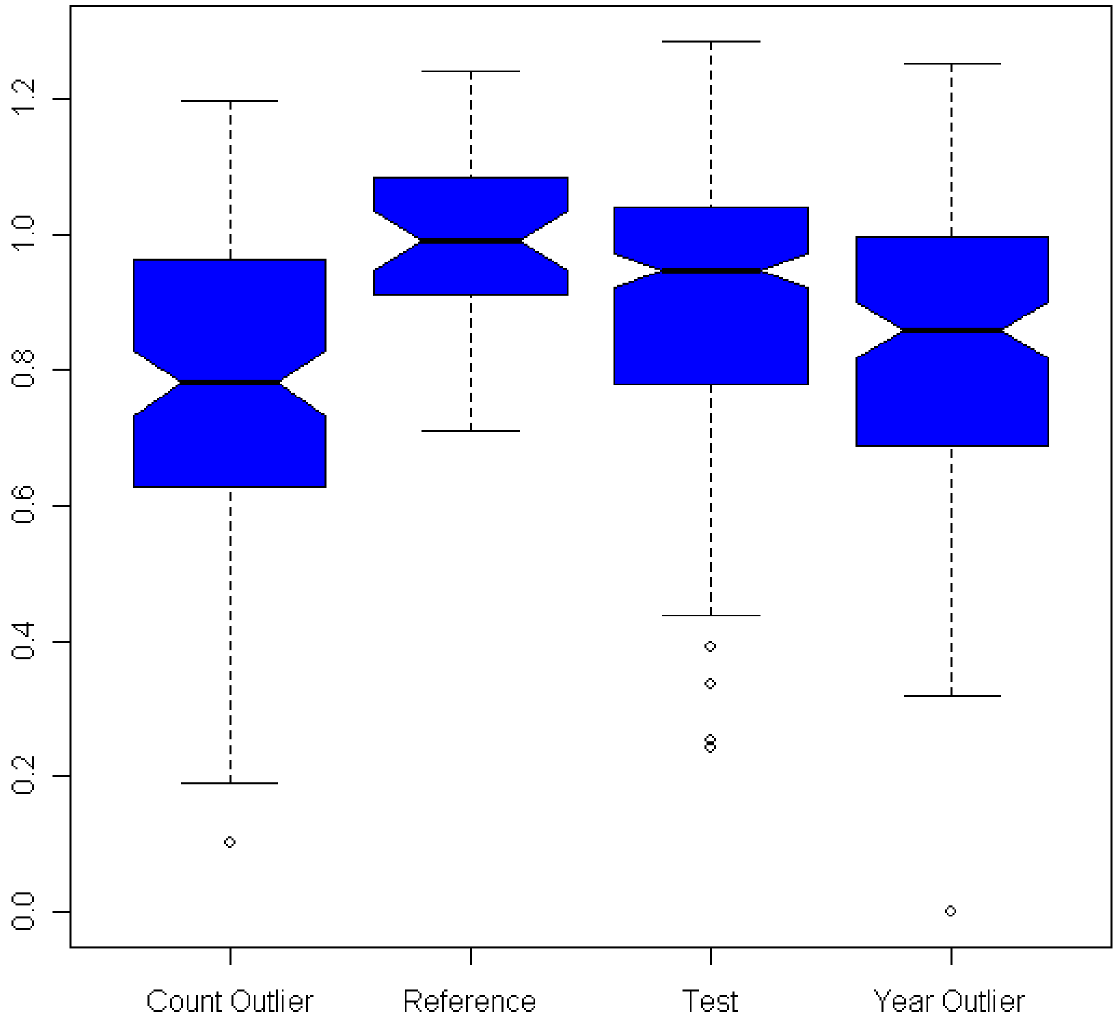


Figure 3. Frequency distributions of O/E scores for samples assessed by the MWCF model. Dark horizontal bands represent the mean for each group. Notches in the boxes are approximations of 95% confidence intervals (±1.58 Inter-quartile Range/(√n)). "Reference" = samples used to build the MWCF model (n=38); "Test" = samples not used to build the model, but within the experience of model constraints (n=252); "Count Outlier" = samples with less than 200 bugs (n=116), "Year Outlier" = samples collected prior to 1998 (n=133).

Benchmarks of biological condition

For PREDATOR's predictive models, the distribution of reference O/E scores is used to establish benchmarks for describing the biological condition of a sample (Table 4). Benchmarks for the predictive models were based on the 10th and 25th percentiles of reference distributions (Turak et. al 1999, Clarke et. al 2003, Ostermiller and Hawkins 2004). An O/E score ≤ 10th percentile of reference scores is considered in "Most disturbed" condition. An O/E score > 10th and ≤ 25th percentiles is considered in "Moderately disturbed" condition. An O/E score > 25th and ≤ 95th is considered in "Least disturbed" condition. Samples with O/E values > 95th percentile of reference sites are considered to be "Enriched". The O/E percentile benchmarks can also be represented as % taxa loss or gain (Table 4).

Table 4. O/E benchmarks for describing biological condition for predictive PREDATOR models. (MWCF = Marine Western Coastal Forest; WC+CP = Western Cordillera + Columbia Plateau.)

Biological Condition Class	Reference percentile	MWCF		WC+CP	
		O/E	% Common Taxa Loss/Gain	O/E	% Common Taxa Loss/Gain
Most disturbed	≤ 10th	≤ 0.85	≥ 15%	≤ 0.78	≥ 22% loss
Moderately disturbed	> 10th to 25th	0.86 - 0.91	9 – 14%	0.79 – 0.92	8 – 21% loss
Least disturbed	> 25th to 95th	0.92 - 1.24	0 - 8% loss 0 - 24% gain	0.93 – 1.23	0 - 7% loss 0 - 23% gain
Enriched	> 95th	> 1.24	> 24 % gain	> 1.23	> 23% gain

Table 5. Benchmarks for describing biological condition for the Northern Basin and Range (NBR) null PREDATOR model.

Biological Condition Class	O/E	% Common Taxa Loss/Gain
Most disturbed	≤ 0.50	≥ 50% loss
Moderately disturbed	> 0.50 to ≤ 0.75	25-49% loss
Least disturbed	> 0.75 to 1.00	< 25% loss
Enriched	> 1.30	> 30% gain

The biological condition of enriched sites is possibly of concern due to the potential for streams to show an increase in diversity as a result of small to moderate levels of disturbance. This concept is known as the intermediate disturbance hypothesis (Ward & Stanford 1983). A high PREDATOR score may be an early warning sign that human activities are altering the macroinvertebrate assemblage, but not yet at a level that has led to assemblage degradation. Alternatively, a high PREDATOR score may simply indicate that a stream reach has exceptionally high richness, potentially representing unique communities worthy of special protection or preserve status.

The choice of these benchmarks was a trade-off between balancing errors in identifying a sample as disturbed when it truly isn't (type I error), or failing to recognize biological disturbance when it exists (type II error) (Sokal and Rohlf 1995). Also, the choice of percentiles was made for consistency with other bioassessment work in this region. Benchmarks such as 1 or 2 standard deviations from the reference site means could also have been chosen. These standard deviations are also statistics that describe the distribution of reference scores and frequently are similar to the percentile benchmarks ultimately chosen.

Due to the low number of reference sites in the NBR (9) and the poor model performance (reference O/E SD = 0.29), the benchmarks for the NBR null model are less stringent than for the predictive models. With so few reference sites, the use of statistics representing the distribution of reference O/E scores did not make sense. Instead, percentages of taxa loss were chosen that match those used in Stoddard et. al (2005). These criteria are more conservative against type-I errors, but less protective of the resource in that type-II errors are much more likely. This points out the need for much more effort in southeastern Oregon (SEOR) to improve DEQ's reference site network and develop better models for this region. Until DEQ develops a more accurate model for SEOR, I recommend using the SEOR null model with caution in bioassessments.

Population Assessments

Example population assessments are shown for all samples assessed in the Coast Range ecoregion and the Willamette Valley ecoregion (Figure 4). The percent of samples (y-axis) which fall below or above the MWCF benchmarks (x-axis) are shown. The results represent the condition of all samples in DEQ's database from the two ecoregions. If the sites were chosen randomly, we could make an estimate of the percent of stream miles in each biotic condition class with error estimates, rather than simply the percent of samples. This would provide an unbiased assessment with quantifiable estimates of error.

With the results shown in Figure 4, it is possible to prioritize future monitoring activities. For instance, there are a substantially lower number of samples collected in the Willamette Valley (35, compared to the Coast Range's 217). With such a small sample size our confidence in the results are diminished. We may want to increase our assessment effort in the Willamette Valley to gain a better understanding of current conditions. (DEQ completed field sampling of a random study design in the Willamette Valley in 2005. Results of this study should be available in 2008.) In the Coast Range, we may want to go back and take additional samples at the locations of the 13% of samples that are “moderately disturbed” and the 1% of samples that are “enriched”, to get a better estimate of biological condition. With repeated sampling, we can determine if these locations are significantly different from reference conditions (see “individual site assessments” below).

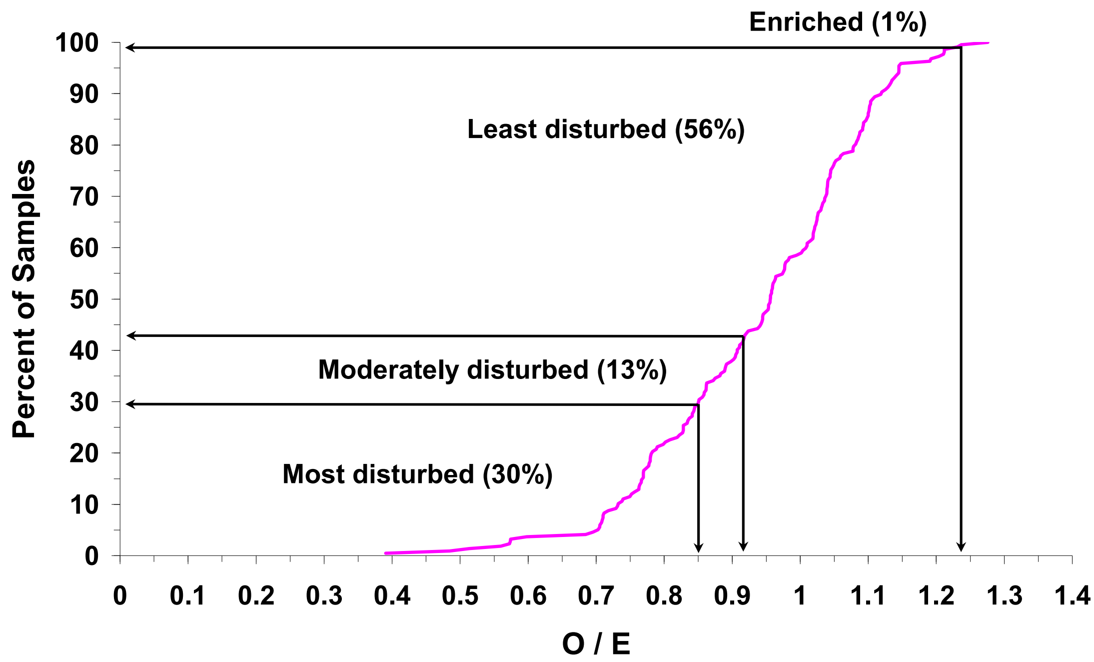
Correlations of PREDATOR scores to environmental variables would be useful in examining patterns of low or high biological condition. Hughes et. al (2004) found the environmental variables most strongly correlated to aquatic vertebrate IBI scores in the Coast Range ecoregion depended on the type of stream. For those streams draining more erosive sedimentary lithology, IBI scores were lower in streams with higher amounts of fine sediments. For streams draining more resistant lithology, road density was most highly associated with low IBI scores. Also shown by Hughes et. al (2004), simple maps of biological condition can be an effective way of presenting patterns of biological condition, as they found pockets of good IBI scores in regions dominated by wilderness or national parks.

Individual site assessments

Assessing biological condition at a single site involves direct comparisons to the mean reference condition. In other words, is the average O/E score at a site significantly different from the reference average? Unlike population assessments where we utilize percentiles of the reference distribution to determine the percent of resource within a given quality category, here the intent is to determine if the biological condition at a single location is significantly different from reference. (It is important to note that the sampling methods employed are designed to represent the macroinvertebrate assemblage within the sampled stream reach, and not the conditions across the larger watershed or landscape. Thus, much care should be exercised in extrapolating results beyond the surveyed reach.)

If a single sample falls below the 10th percentile of the reference distribution, the sample is considered to be outside the reference distribution. We feel confident that a single sample score below the 10th percentile is not different simply by chance, but rather a true difference in biological condition exists (assuming the site is not an outlier for any reason). In this case, a single sample is sufficient to classify the stream reach as biologically disturbed, or “not supporting” the beneficial use. However, if a sample falls between the 10th and 25th percentiles of the reference distribution (“moderately disturbed”), there is less confidence that the O/E score is outside of the reference distribution. In this case, DEQ recommends repeated measures of O/E to determine if a significant difference in biological condition exists. We also recommend assessments include surveys of water quality, instream and riparian habitat, and remote sensing of the watershed (GIS) to provide insights into possible sources of disturbance. A site with a “most disturbed” O/E score and minimal signs of human influences may indicate that the site was not accurately modeled with the current set of reference sites. These are important findings that may be used to increase the future accuracy of predicting locally common reference taxa.

A



B

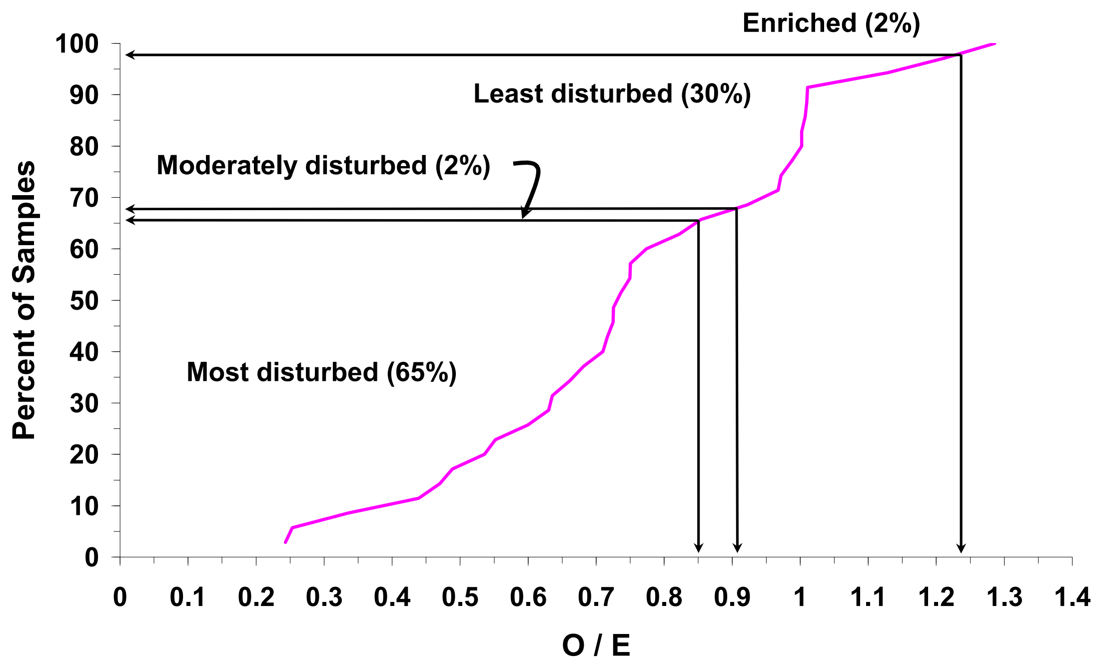


Figure 4. The extent of biotic condition classes for samples in the Coast Range ecoregion (panel A, n=217) and the Willamette Valley ecoregion (panel B, n=35). Vertical lines are the 10th, 25th, and 95th percentiles (from left to right, respectively) of MWCF reference O/E scores (n = 217).

For a sample with higher than expected O/E (enriched), determining biological condition would also require further monitoring of the stream and its watershed. First, a combination of on-site (field observations) and remote sensing (GIS) screens of the watershed could be performed to identify potential sources of human disturbances. Those sites with levels of human disturbances similar to regional reference sites may be deemed naturally enriched. Those with higher levels of human activities may require further field sampling to determine if the existing activities are affecting the beneficial use. Repeated macroinvertebrate sampling, sampling for water quality, and instream and riparian habitat sampling may provide additional information concerning potential causes of disturbance.

Causes of poor biological condition

Identifying biological condition does not satisfy all bioassessment needs. Knowing a site is in poor biological condition is useful, but unless we are able to identify the cause(s) of impairment, we are at a loss for how to *most effectively* go about improving the stream.

Information on tolerances from individual taxa can be paired with the information from PREDATOR to get a sense of the likelihood of each variable as a potential cause of poor biological condition. DEQ has developed optima and tolerances for macroinvertebrate taxa to both seasonal maximum temperature and percent fine sediments (Huff et. al 2006).

The “Probability Matrix” output from the WCM shows missing taxa (they were expected to occur, but were not collected) and replacement taxa (they were not expected to occur, but were collected). With information regarding individual taxa sensitivities (optima and tolerances) to different stressors, it is possible to tease out possible causes of disturbance. In Figure 5, two streams in most disturbed condition (PREDATOR O/E < 0.85) are shown. Poor biological condition in Lower Mill Creek may be related to temperature. The missing taxa show lower temperature optima (~16-17 °C) compared to the collected (~17-18 °C) and replacement (~16.5-21 °C). On the other hand, replacement taxa show a very broad range of fine sediment optima, both lower and higher than collected and missing taxa. At Panther Creek, poor biological condition appears to be related to fine sediments. The missing and replacement taxa optima are nearly identical, and overlap the collected taxa optima. Fine sediment optima are much higher for replacement taxa (~9-18 °C) than missing taxa (~6-9 °C) and collected taxa (~8-10 °C).

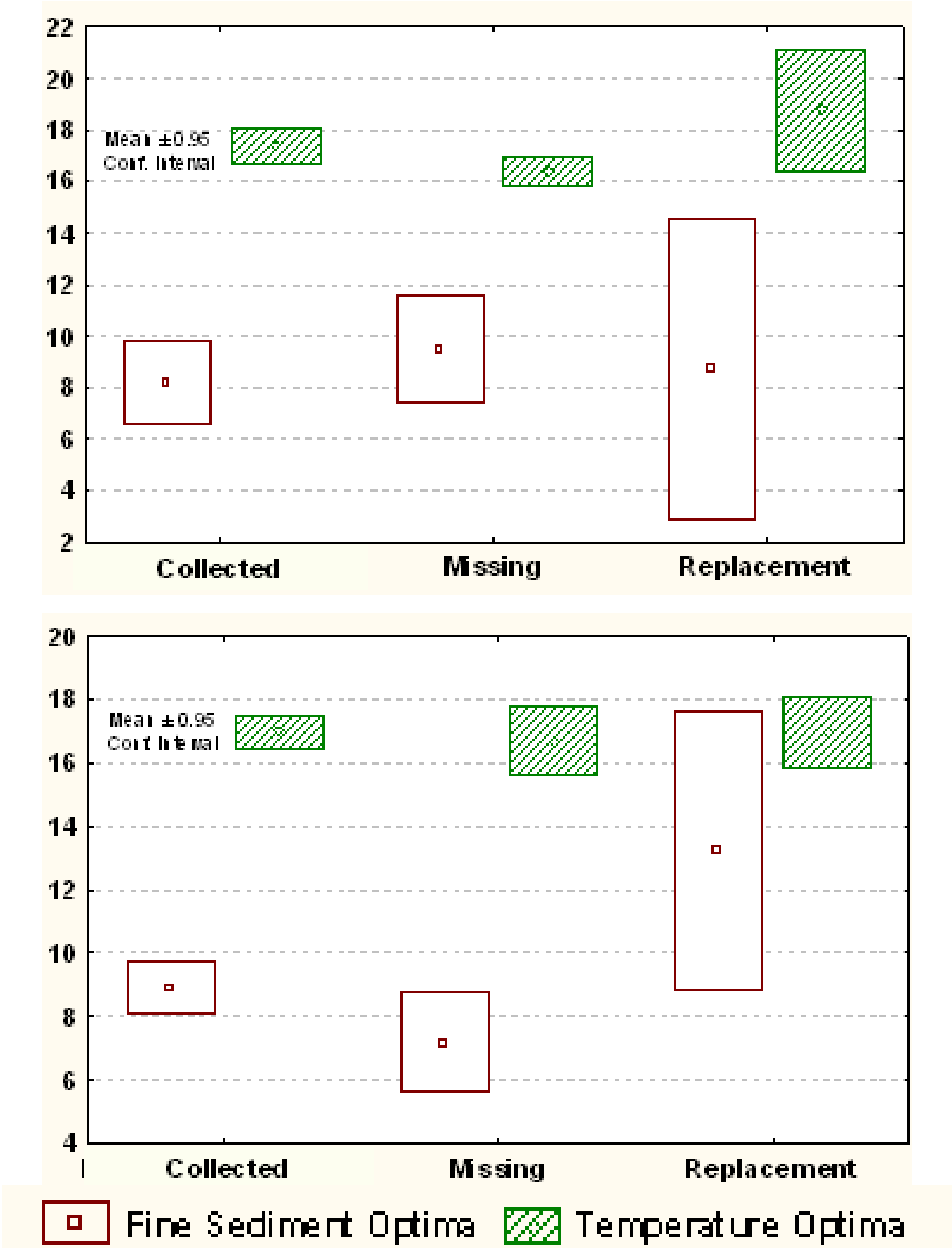


Figure 5. Identifying potential causes of impairment in two sites with O/E in most disturbed condition. The graphs show sites where poor biological condition is potentially related to temperature (panel A) and fine sediment (panel B). Optima for individual taxa were calculated with weighted averaging (Huff et. al 2006). The horizontal axis represents both percent fine sediments and temperature (^{o}C).

The importance of assessing multiple assemblages

When assessing the condition of a study area it would be wise to include the results of the conditions of multiple assemblages. Different assemblages may respond differently to various stressors. If we wanted to assess chemical water quality in a region, we would measure multiple parameters and not just dissolved oxygen. Similarly, it may be unwise to base our conclusions of the overall biological condition in a region entirely on the results of one assemblage.

An assessment of aquatic vertebrate assemblages in the Coast Range ecoregion showed 45% of stream miles in most disturbed conditions (Hughes et. al 2004), while Figure 4 shows 30% of macroinvertebrate samples are most disturbed. Direct comparisons are difficult because Hughes et. al uses a random study design and slightly different condition class benchmarks. Combining information from both assemblages would allow for more robust decisions to be made on the current status of biological condition, as well as the direction of future resource management in the Coast Range.

Not only can multiple assemblages show varying levels of the resource in disturbed condition, they can also show varying responses to stressors. DEQ (2005) assessed the biological condition of aquatic vertebrates and macroinvertebrates in the Coastal Coho Evolutionarily Significant Unit (ESU), which overlaps considerably with the Coast Range ecoregion, from 1994-2003. Both assemblages showed similar amounts of stream resource in most disturbed biological condition (28% and 36%, respectively). However, when the major stressors affecting each community were assessed (relative risk, Van Sickle et. al 2006), they found macroinvertebrates were significantly affected by high levels of fine sediment, while aquatic vertebrates showed an insignificant response.

A similar study in the Lower Columbia ESU, DEQ (2007) showed a much higher percentage of stream miles in most disturbed condition for aquatic vertebrates than macroinvertebrates (22% and 7%, respectively). Of all the stressors showing significant risks to either assemblage, only three stressors were not significantly affecting both assemblages. Low dissolved oxygen, higher human disturbances in the riparian, and lower canopy condition showed significant affects on vertebrate condition, but not on macroinvertebrate condition. The other significant stressors consistently showed ~10x greater risk to macroinvertebrate assemblages than aquatic vertebrates. These results suggest it is important to look at multiple assemblages to fully assess the amount of stream resource in peril (most disturbed condition), as well as what types of stressors are responsible for the poor biological conditions.

Conclusions

DEQ developed three regional models (PREDATOR) that can be used to assess biotic condition of Oregon's wadeable streams using macroinvertebrates. Two of these models are predictive models, while the third is a null model with no predictive component. We attempted to build predictive models that would be able to assess all wadeable streams in Oregon, but model performance decreased significantly when macroinvertebrate samples from reference sites in southeastern Oregon were included.

There are several important considerations for using PREDATOR models. Those wishing to utilize PREDATOR should carefully consider the implications of scoring samples taken outside of the context of the models. Failure to follow the specifications of each PREDATOR model may lead to inappropriate interpretations of biotic condition.

Those ecoregions where DEQ currently has abundant reference sites have had large scale monitoring efforts within them (Cascades, Coast Range, and Blue Mountains). However, there are several ecoregions where DEQ's reference samples are limited (Willamette Valley, East Cascades, Columbia Plateau, Klamath Mountains, and Northern Basin and Range, Snake River Plains). Precision in assessments of biotic condition in these regions would likely be improved by increasing the monitoring effort in these regions, as well as polling neighboring states for potential reference sites.

In addition to increasing the reference site pool for those ecoregions with relatively few selected sites, DEQ should develop and maintain a long-term reference site sampling plan. We need to be able to assess whether or not biological assemblages at reference sites are stable, or if they are changing through time. If they are changing—that is O/E scores at reference sites are significantly different from those original calibration set—then we need to re-model. Without monitoring a subset of the reference sites periodically, we will not have a good understanding of how well the models work under future conditions. Given the potential for climate change to impact stream communities (e.g., decreased streamflow, increased temperature, etc.), it is important to adopt measures that allow for long-term assessment of PREDATOR's effectiveness. Finally, it would make sense to implement a statewide network of reference sites where resource management and land activities can remain relatively consistent. If we allow increased human activities or disturbances in reference watersheds, then future measurements at these sites will likely show a degradation of reference sites' biological condition.

Future versions of PREDATOR

As new reference sites are sampled, the models will be re-examined with the intent of improving our assessments in poorly represented regions. Incorporation of more reference sites will provide additional statistical precision in O/E scores by assessing model performance using independent reference datasets. Since 2004, DEQ has collected reference macroinvertebrate samples from western Oregon, especially in the Klamath Mountains ecoregion. Additionally, DEQ should partner with neighboring states to share reference sites, not only for RIVPACS-type models, but also for establishing reference benchmarks for water chemistry and physical habitat attributes from streams and rivers.

Future versions of PREDATOR may change the environmental predictor variables if additional reference site data shows this is necessary. New statistical procedures, such as Random Forests and Classification and Regression Tree models (Cao et. al 2007), may allow for more precise models. Ultimately, DEQ is interested in making sure the PREDATOR models are available and easy to use for as wide an audience as possible, while achieving maximum model performance.

Recommendations and Needs

1) Periodic sampling of reference sites used to build the models.

2) Increased monitoring in southeastern Oregon and the Columbia Plateau ecoregion. (Both random surveys and targeted reference sampling.)

3) Obtain reference sites from neighboring states—especially in regions where DEQ currently lacks adequate reference data sets.

4) Resources to educate and train third parties interested in using PREDATOR.

5) Develop accurate, precise, and sensitive models or indices for algae, aquatic vertebrates, and macroinvertebrates that can assess the biological condition of all stream and rivers in Oregon.

Acknowledgements

Dave Huff of the University of Minnesota was instrumental in building the PREDATOR models. Chuck Hawkins and Mark Vinson of Utah State University and Rob Plotnikoff of Washington Department of Ecology for providing data used to build the models. John Van Sickle of USEPA's Office of Research and Development provided R-code which has vastly improved our ability to create and assess model performance, as well as a review of this document. Bob Hughes of Oregon State University provided an excellent critique of this paper. The Oregon Watershed Enhancement Board for funding that allowed Jeff Adams of the Xerces Society to pull together training materials.

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Appendix A.

Table 6. OTUs and (abbreviated) phylogenetic classifications used in the November 2005 PREDATOR models.

Phylum	Class	Order	Family	Subfamily	Tribe	OTU
Annelida	Hirudinea					Hirudinea
Annelida	Oligochaeta					Oligochaeta
Arthropoda	Arachnoidea	Sarcoptiformes	Oribatidae			Trombidiformes
Arthropoda	Arachnoidea	Trombidiformes	"Hydracarina"			Trombidiformes
Arthropoda	Crustacea	Amphipoda	Crangonyctidae			Crangonyx
Arthropoda	Crustacea	Amphipoda	Crangonyctidae			Stygobromus
Arthropoda	Crustacea	Amphipoda	Gammaridae			Eogammarus
Arthropoda	Crustacea	Amphipoda	Gammaridae			Gammarus
Arthropoda	Crustacea	Amphipoda	Gammaridae			Ramellogammarus
Arthropoda	Crustacea	Amphipoda	Hyalellidae			Hyalella
Arthropoda	Crustacea	Amphipoda	Talitridae			Hyalella
Arthropoda	Crustacea	Isopoda				Asellidae
Arthropoda	Crustacea	Podocopa				Ostracoda
Arthropoda	Insecta	Coleoptera	Amphizoidae			Amphizoa
Arthropoda	Insecta	Coleoptera	Chrysomelidae			Chrysomelidae
Arthropoda	Insecta	Coleoptera	Curculionidae			Curculionidae
Arthropoda	Insecta	Coleoptera	Dryopidae			Helichus
Arthropoda	Insecta	Coleoptera	Dytiscidae			Dytiscidae
Arthropoda	Insecta	Coleoptera	Elmidae			Ampumixis
Arthropoda	Insecta	Coleoptera	Elmidae			Atractelmis_wawona
Arthropoda	Insecta	Coleoptera	Elmidae			Cleptelmis
Arthropoda	Insecta	Coleoptera	Elmidae			Cylloepus

Phylum	Class	Order	Family	Subfamily	Tribe	OTU
Arthropoda	Insecta	Coleoptera	Elmidae			Dubiraphia
Arthropoda	Insecta	Coleoptera	Elmidae			Heterelmis
Arthropoda	Insecta	Coleoptera	Elmidae			Heterlimnius
Arthropoda	Insecta	Coleoptera	Elmidae			Lara
Arthropoda	Insecta	Coleoptera	Elmidae			Microcylloepus
Arthropoda	Insecta	Coleoptera	Elmidae			Narpus
Arthropoda	Insecta	Coleoptera	Elmidae			Optioservus
Arthropoda	Insecta	Coleoptera	Elmidae			Ordobrevia
Arthropoda	Insecta	Coleoptera	Elmidae			Rhizelmis
Arthropoda	Insecta	Coleoptera	Elmidae			Stenelmis
Arthropoda	Insecta	Coleoptera	Elmidae			Zaitzevia
Arthropoda	Insecta	Coleoptera	Haliplidae			Haliplidae
Arthropoda	Insecta	Coleoptera	Hydraenidae			Hydraenidae
Arthropoda	Insecta	Coleoptera	Hydrochidae			Hydrochus
Arthropoda	Insecta	Coleoptera	Hydrophilidae			Hydrophilidae
Arthropoda	Insecta	Coleoptera	Noteridae			Noteridae
Arthropoda	Insecta	Coleoptera	Psephenidae			Acneus
Arthropoda	Insecta	Coleoptera	Psephenidae			Dicranopselaphus
Arthropoda	Insecta	Coleoptera	Psephenidae			Eubrianax_edwardsi
Arthropoda	Insecta	Coleoptera	Psephenidae			Psephenus
Arthropoda	Insecta	Coleoptera	Ptilodactylidae			Ptilodactylidae
Arthropoda	Insecta	Coleoptera	Scirtidae			Scirtidae
Arthropoda	Insecta	Coleoptera	Staphylinidae			Staphylinidae
Arthropoda	Insecta	Diptera	Athericidae			Atherix

Phylum	Class	Order	Family	Subfamily	Tribe	OTU
Arthropoda	Insecta	Diptera	Blephariceridae			Blephariceridae
Arthropoda	Insecta	Diptera	Ceratopogonidae	Ceratopogoninae		Ceratopogoninae
Arthropoda	Insecta	Diptera	Ceratopogonidae	Dasyheleinae		Dasyheleinae
Arthropoda	Insecta	Diptera	Ceratopogonidae	Forcipomyiinae		Forcipomyiinae
Arthropoda	Insecta	Diptera	Chaoboridae			Chaoboridae
Arthropoda	Insecta	Diptera	Chironomidae	Chironominae		Chironominae
Arthropoda	Insecta	Diptera	Chironomidae	Diamesinae		Diamesinae
Arthropoda	Insecta	Diptera	Chironomidae	Orthocladiinae		Orthocladiinae
Arthropoda	Insecta	Diptera	Chironomidae	Podonominae		Podonominae
Arthropoda	Insecta	Diptera	Chironomidae	Prodiamesinae		Prodiamesinae
Arthropoda	Insecta	Diptera	Chironomidae	Tanypodinae		Tanypodinae
Arthropoda	Insecta	Diptera	Culicidae			Culicidae
Arthropoda	Insecta	Diptera	Deuterophlebiidae			Deuterophlebia
Arthropoda	Insecta	Diptera	Dixidae			Dixa
Arthropoda	Insecta	Diptera	Dixidae			Dixella
Arthropoda	Insecta	Diptera	Dixidae			Meringodixa
Arthropoda	Insecta	Diptera	Dolichopodidae			Dolichopodidae
Arthropoda	Insecta	Diptera	Empididae			Chelifera_
Arthropoda	Insecta	Diptera	Empididae			Clinocera
Arthropoda	Insecta	Diptera	Empididae			Hemerodromia
Arthropoda	Insecta	Diptera	Empididae			Neoplasta
Arthropoda	Insecta	Diptera	Empididae			Oreogeton
Arthropoda	Insecta	Diptera	Empididae			Phyllodromia
Arthropoda	Insecta	Diptera	Empididae			Trichoclinocera

Phylum	Class	Order	Family	Subfamily	Tribe	OTU
Arthropoda	Insecta	Diptera	Empididae			Wiedemannia
Arthropoda	Insecta	Diptera	Ephydridae			Ephydridae
Arthropoda	Insecta	Diptera	Muscidae			Muscidae
Arthropoda	Insecta	Diptera	Pelecorhynchidae			Glutops
Arthropoda	Insecta	Diptera	Phoridae			Phoridae
Arthropoda	Insecta	Diptera	Psychodidae			Maruina
Arthropoda	Insecta	Diptera	Psychodidae			Pericoma/Telmatoscopus
Arthropoda	Insecta	Diptera	Psychodidae			Psychoda
Arthropoda	Insecta	Diptera	Ptychopteridae			Ptychopteridae
Arthropoda	Insecta	Diptera	Sciomyzidae			Sciomyzidae
Arthropoda	Insecta	Diptera	Simuliidae			Prosimulium
Arthropoda	Insecta	Diptera	Simuliidae			Simulium
Arthropoda	Insecta	Diptera	Simuliidae			Twinnia
Arthropoda	Insecta	Diptera	Stratiomyidae			Stratiomyidae
Arthropoda	Insecta	Diptera	Syrphidae			Syrphidae
Arthropoda	Insecta	Diptera	Tabanidae			Tabanidae
Arthropoda	Insecta	Diptera	Tanyderidae			Tanyderidae
Arthropoda	Insecta	Diptera	Thaumaleidae			Thaumalea
Arthropoda	Insecta	Diptera	Tipulidae			Ulomorpha
Arthropoda	Insecta	Diptera	Tipulidae	Limoniinae		Antocha
Arthropoda	Insecta	Diptera	Tipulidae	Limoniinae		Cryptolabis
Arthropoda	Insecta	Diptera	Tipulidae	Limoniinae		Dicranota
Arthropoda	Insecta	Diptera	Tipulidae	Limoniinae		Erioptera
Arthropoda	Insecta	Diptera	Tipulidae	Limoniinae		Gonomyia

Phylum	Class	Order	Family	Subfamily	Tribe	OTU
Arthropoda	Insecta	Diptera	Tipulidae	Limoniinae		Gonomyodes
Arthropoda	Insecta	Diptera	Tipulidae	Limoniinae		Hesperoconopa
Arthropoda	Insecta	Diptera	Tipulidae	Limoniinae		Hexatoma
Arthropoda	Insecta	Diptera	Tipulidae	Limoniinae		Limnophila
Arthropoda	Insecta	Diptera	Tipulidae	Limoniinae		Limonia
Arthropoda	Insecta	Diptera	Tipulidae	Limoniinae		Molophilus
Arthropoda	Insecta	Diptera	Tipulidae	Limoniinae		Ormosia
Arthropoda	Insecta	Diptera	Tipulidae	Limoniinae		Pedicia
Arthropoda	Insecta	Diptera	Tipulidae	Limoniinae		Pilaria
Arthropoda	Insecta	Diptera	Tipulidae	Limoniinae		Rhabdomastix
Arthropoda	Insecta	Diptera	Tipulidae	Tipulinae		Tipula
Arthropoda	Insecta	Ephemeroptera	Ameletidae			Ameletus
Arthropoda	Insecta	Ephemeroptera	Baetidae			Acentrella
Arthropoda	Insecta	Ephemeroptera	Baetidae			Acerpenna
Arthropoda	Insecta	Ephemeroptera	Baetidae			Apobaetis_indeprensus
Arthropoda	Insecta	Ephemeroptera	Baetidae			Baetis
Arthropoda	Insecta	Ephemeroptera	Baetidae			Callibaetis
Arthropoda	Insecta	Ephemeroptera	Baetidae			Camelobaetidius
Arthropoda	Insecta	Ephemeroptera	Baetidae			Centroptilum
Arthropoda	Insecta	Ephemeroptera	Baetidae			Diphetor_hageni
Arthropoda	Insecta	Ephemeroptera	Baetidae			Fallceon_quilleri
Arthropoda	Insecta	Ephemeroptera	Baetidae			Heterocloeon_anoka
Arthropoda	Insecta	Ephemeroptera	Baetidae			Maccaffertium_terminatum
Arthropoda	Insecta	Ephemeroptera	Baetidae			Maccaffertium_vicarium

Phylum	Class	Order	Family	Subfamily	Tribe	OTU
Arthropoda	Insecta	Ephemeroptera	Baetidae			Paracloeodes_minutus
Arthropoda	Insecta	Ephemeroptera	Baetidae			Plauditus
Arthropoda	Insecta	Ephemeroptera	Baetidae			Procloeon
Arthropoda	Insecta	Ephemeroptera	Baetidae			Pseudocloeon
Arthropoda	Insecta	Ephemeroptera	Caenidae			Caenis
Arthropoda	Insecta	Ephemeroptera	Ephemerellidae			Eurylophella
Arthropoda	Insecta	Ephemeroptera	Ephemerellidae	Ephemerellinae		Attenella
Arthropoda	Insecta	Ephemeroptera	Ephemerellidae	Ephemerellinae		Caudatella
Arthropoda	Insecta	Ephemeroptera	Ephemerellidae	Ephemerellinae		Drunella_coloradensis/flavilinea
Arthropoda	Insecta	Ephemeroptera	Ephemerellidae	Ephemerellinae		Drunella_doddsi
Arthropoda	Insecta	Ephemeroptera	Ephemerellidae	Ephemerellinae		Drunella_grandis
Arthropoda	Insecta	Ephemeroptera	Ephemerellidae	Ephemerellinae		Drunella_pelosa
Arthropoda	Insecta	Ephemeroptera	Ephemerellidae	Ephemerellinae		Drunella_spinifera
Arthropoda	Insecta	Ephemeroptera	Ephemerellidae	Ephemerellinae		Ephemerella
Arthropoda	Insecta	Ephemeroptera	Ephemerellidae	Ephemerellinae		Serratella
Arthropoda	Insecta	Ephemeroptera	Ephemerellidae	Timpanoginae		Timpanoga_hecuba
Arthropoda	Insecta	Ephemeroptera	Ephemeridae			Ephemeridae
Arthropoda	Insecta	Ephemeroptera	Heptageniidae	Heptageniinae		Cinygma
Arthropoda	Insecta	Ephemeroptera	Heptageniidae	Heptageniinae		Cinygmula
Arthropoda	Insecta	Ephemeroptera	Heptageniidae	Heptageniinae		Epeorus
Arthropoda	Insecta	Ephemeroptera	Heptageniidae	Heptageniinae		Heptagenia
Arthropoda	Insecta	Ephemeroptera	Heptageniidae	Heptageniinae		Ironodes
Arthropoda	Insecta	Ephemeroptera	Heptageniidae	Heptageniinae		Nixe/Leucocruta
Arthropoda	Insecta	Ephemeroptera	Heptageniidae	Heptageniinae		Rhithrogena

Phylum	Class	Order	Family	Subfamily	Tribe	OTU
Arthropoda	Insecta	Ephemeroptera	Heptageniidae	Heptageniinae		Stenonema
Arthropoda	Insecta	Ephemeroptera	Isonychiidae			Isonychiidae
Arthropoda	Insecta	Ephemeroptera	Leptohyphidae			Asioplax
Arthropoda	Insecta	Ephemeroptera	Leptophlebiidae			Leptophlebiidae
Arthropoda	Insecta	Ephemeroptera	Polymitarcydae			Polymitarcydae
Arthropoda	Insecta	Ephemeroptera	Siphlonuridae			Siphlonuridae
Arthropoda	Insecta	Ephemeroptera	Tricorythidae			Tricorythodes
Arthropoda	Insecta	Hemiptera	Belostomatidae			Belostomatidae
Arthropoda	Insecta	Lepidoptera				Petrophila
Arthropoda	Insecta	Lepidoptera	Pyralidae			Petrophila
Arthropoda	Insecta	Megaloptera	Corydalidae			Corydalidae
Arthropoda	Insecta	Megaloptera	Sialidae			Sialis
Arthropoda	Insecta	Neuroptera	Sisyridae			Sisyridae
Arthropoda	Insecta	Odonata	Aeshnidae			Aeshnidae
Arthropoda	Insecta	Odonata	Calopterygidae			Calopterygidae
Arthropoda	Insecta	Odonata	Coenagrionidae			Coenagrionidae
Arthropoda	Insecta	Odonata	Cordulegastridae			Cordulegaster
Arthropoda	Insecta	Odonata	Corduliidae			Corduliidae
Arthropoda	Insecta	Odonata	Gomphidae			Gomphidae
Arthropoda	Insecta	Odonata	Lestidae			Lestidae
Arthropoda	Insecta	Odonata	Libellulidae			Libellulidae
Arthropoda	Insecta	Plecoptera	Capniidae			Capniidae
Arthropoda	Insecta	Plecoptera	Capniidae	Capniinae		Capniidae
Arthropoda	Insecta	Plecoptera	Chloroperlidae	Chloroperlinae		Neaviperla

Phylum	Class	Order	Family	Subfamily	Tribe	OTU
Arthropoda	Insecta	Plecoptera	Chloroperlidae	Chloroperlinae	Alloperlini	Alloperla
Arthropoda	Insecta	Plecoptera	Chloroperlidae	Chloroperlinae	Alloperlini	Sweltsa
Arthropoda	Insecta	Plecoptera	Chloroperlidae	Chloroperlinae	Chloroperlini	Haploperla
Arthropoda	Insecta	Plecoptera	Chloroperlidae	Chloroperlinae	Chloroperlini	Plumiperla
Arthropoda	Insecta	Plecoptera	Chloroperlidae	Chloroperlinae	Suwallini	Suwallia
Arthropoda	Insecta	Plecoptera	Chloroperlidae	Paraperlinae		Kathroperla
Arthropoda	Insecta	Plecoptera	Chloroperlidae	Paraperlinae		Paraperla
Arthropoda	Insecta	Plecoptera	Chloroperlidae	Paraterlinae		Utaperla
Arthropoda	Insecta	Plecoptera	Leuctridae	Leuctrinae		Despaxia
Arthropoda	Insecta	Plecoptera	Leuctridae	Leuctrinae		Leuctra
Arthropoda	Insecta	Plecoptera	Leuctridae	Leuctrinae		Moselia
Arthropoda	Insecta	Plecoptera	Leuctridae	Leuctrinae		Paraleuctra
Arthropoda	Insecta	Plecoptera	Leuctridae	Leuctrinae		Perlomyia
Arthropoda	Insecta	Plecoptera	Leuctridae	Megaleuctrinae		Megaleuctra
Arthropoda	Insecta	Plecoptera	Nemouridae	Amphinemurinae		Malenka
Arthropoda	Insecta	Plecoptera	Nemouridae	Nemourinae		Nemoura
Arthropoda	Insecta	Plecoptera	Nemouridae	Nemourinae		Ostrocerca
Arthropoda	Insecta	Plecoptera	Nemouridae	Nemourinae		Podmosta
Arthropoda	Insecta	Plecoptera	Nemouridae	Nemourinae		Prostoia
Arthropoda	Insecta	Plecoptera	Nemouridae	Nemourinae		Soyedina
Arthropoda	Insecta	Plecoptera	Nemouridae	Nemourinae		Visoka
Arthropoda	Insecta	Plecoptera	Nemouridae	Nemourinae		Zapada
Arthropoda	Insecta	Plecoptera	Peltoperlidae	Peltoperlinae		Sierraperla
Arthropoda	Insecta	Plecoptera	Peltoperlidae	Peltoperlinae		Soliperla
Arthropoda	Insecta	Plecoptera	Peltoperlidae	Peltoperlinae		Yoraperla

Phylum	Class	Order	Family	Subfamily	Tribe	OTU
Arthropoda	Insecta	Plecoptera	Perlidae			Perlesta
Arthropoda	Insecta	Plecoptera	Perlidae	Acroneuriinae	Acroneurini	Acroneuria
Arthropoda	Insecta	Plecoptera	Perlidae	Acroneuriinae	Acroneurini	Calineuria
Arthropoda	Insecta	Plecoptera	Perlidae	Acroneuriinae	Acroneurini	Doroneuria
Arthropoda	Insecta	Plecoptera	Perlidae	Acroneuriinae	Acroneurini	Hesperoperla
Arthropoda	Insecta	Plecoptera	Perlidae	Perlinae	Perlini	Claassenia
Arthropoda	Insecta	Plecoptera	Perlodidae	Isoperlinae		Calliperla
Arthropoda	Insecta	Plecoptera	Perlodidae	Isoperlinae		Cascadoperla
Arthropoda	Insecta	Plecoptera	Perlodidae	Isoperlinae		Isoperla
Arthropoda	Insecta	Plecoptera	Perlodidae	Perlodinae	Arcynopterygini	Frisonia
Arthropoda	Insecta	Plecoptera	Perlodidae	Perlodinae	Arcynopterygini	Megarcys
Arthropoda	Insecta	Plecoptera	Perlodidae	Perlodinae	Arcynopterygini	Oroperla
Arthropoda	Insecta	Plecoptera	Perlodidae	Perlodinae	Arcynopterygini	Perlinodes
Arthropoda	Insecta	Plecoptera	Perlodidae	Perlodinae	Arcynopterygini	Setvena
Arthropoda	Insecta	Plecoptera	Perlodidae	Perlodinae	Arcynopterygini	Skwala
Arthropoda	Insecta	Plecoptera	Perlodidae	Perlodinae	Diploperlini	Cultus
Arthropoda	Insecta	Plecoptera	Perlodidae	Perlodinae	Diploperlini	Kogotus
Arthropoda	Insecta	Plecoptera	Perlodidae	Perlodinae	Diploperlini	Osobenus
Arthropoda	Insecta	Plecoptera	Perlodidae	Perlodinae	Diploperlini	Pictetiella
Arthropoda	Insecta	Plecoptera	Perlodidae	Perlodinae	Diploperlini	Rickera
Arthropoda	Insecta	Plecoptera	Perlodidae	Perlodinae	Perlodini	Diura
Arthropoda	Insecta	Plecoptera	Perlodidae	Perlodinae	Perlodini	Isogenoides
Arthropoda	Insecta	Plecoptera	Pteronarcyidae	Pteronarcyinae	Pteronarcellini	Pteronarcella
Arthropoda	Insecta	Plecoptera	Pteronarcyidae	Pteronarcyinae	Pteronarcyini	Pteronarcys
Arthropoda	Insecta	Plecoptera	Taeniopterygidae			Taeniopterygidae
Arthropoda	Insecta	Trichoptera	Apataniidae			Allomyia
Arthropoda	Insecta	Trichoptera	Apataniidae			Moselyana

Phylum	Class	Order	Family	Subfamily	Tribe	OTU
Arthropoda	Insecta	Trichoptera	Apataniidae			Pedomoecus
Arthropoda	Insecta	Trichoptera	Apataniidae	Apataniinae		Apatania
Arthropoda	Insecta	Trichoptera	Brachycentridae			Amiocentrus
Arthropoda	Insecta	Trichoptera	Brachycentridae			Brachycentrus
Arthropoda	Insecta	Trichoptera	Brachycentridae			Micrasema
Arthropoda	Insecta	Trichoptera	Calamoceratidae	Calamoceratinae		Heteroplectron
Arthropoda	Insecta	Trichoptera	Glossosomatidae	Agapetinae		Agapetus
Arthropoda	Insecta	Trichoptera	Glossosomatidae	Glossosomatinae	Anagapetini	Anagapetus
Arthropoda	Insecta	Trichoptera	Glossosomatidae	Glossosomatinae	Glossosomatini	Glossosoma
Arthropoda	Insecta	Trichoptera	Glossosomatidae	Protoptilinae		Culoptila
Arthropoda	Insecta	Trichoptera	Glossosomatidae	Protoptilinae		Protoptila
Arthropoda	Insecta	Trichoptera	Goeridae	Goerinae		Goera
Arthropoda	Insecta	Trichoptera	Goeridae	Goerinae		Goeracea
Arthropoda	Insecta	Trichoptera	Helicopsychidae			Helicopsyche
Arthropoda	Insecta	Trichoptera	Hydropsychidae	Arctopsychinae		Arctopsyche
Arthropoda	Insecta	Trichoptera	Hydropsychidae	Arctopsychinae		Parapsyche
Arthropoda	Insecta	Trichoptera	Hydropsychidae	Hydropsychinae		Cheumatopsyche
Arthropoda	Insecta	Trichoptera	Hydropsychidae	Hydropsychinae		Hydropsyche
Arthropoda	Insecta	Trichoptera	Hydroptilidae			Ithytrichia
Arthropoda	Insecta	Trichoptera	Hydroptilidae	Hydroptilinae	Hydroptilini	Agraylea
Arthropoda	Insecta	Trichoptera	Hydroptilidae	Hydroptilinae	Hydroptilini	Hydroptila
Arthropoda	Insecta	Trichoptera	Hydroptilidae	Hydroptilinae	Hydroptilini	Oxyethira
Arthropoda	Insecta	Trichoptera	Hydroptilidae	Hydroptilinae	Hydroptilini	Paucicalcaria
Arthropoda	Insecta	Trichoptera	Hydroptilidae	Hydroptilinae	Leucotrichiini	Leucotrichia
Arthropoda	Insecta	Trichoptera	Hydroptilidae	Hydroptilinae	Neotrichiini	Neotrichia

Phylum	Class	Order	Family	Subfamily	Tribe	OTU
Arthropoda	Insecta	Trichoptera	Hydroptilidae	Hydroptilinae	Ochrottrichiini	Metrichia
Arthropoda	Insecta	Trichoptera	Hydroptilidae	Hydroptilinae	Ochrottrichiini	Ochrotrichia
Arthropoda	Insecta	Trichoptera	Hydroptilidae	Hydroptilinae	Stactobiini	Alisotrichia
Arthropoda	Insecta	Trichoptera	Hydroptilidae	Hydroptilinae	Stactobiini	Stactobiella
Arthropoda	Insecta	Trichoptera	Hydroptilidae	Ptilocolepinae		Palaegapetus
Arthropoda	Insecta	Trichoptera	Lepidostomatidae			Lepidostoma
Arthropoda	Insecta	Trichoptera	Lepidostomatidae	Lepidostomatinae		Lepidostoma
Arthropoda	Insecta	Trichoptera	Leptoceridae			Mystacides
Arthropoda	Insecta	Trichoptera	Leptoceridae	Leptocerinae	Athripsodini	Ceraclea
Arthropoda	Insecta	Trichoptera	Leptoceridae	Leptocerinae	Mystacidini	Mystacides
Arthropoda	Insecta	Trichoptera	Leptoceridae	Leptocerinae	Nectopsychini	Nectopsyche
Arthropoda	Insecta	Trichoptera	Leptoceridae	Leptocerinae	Oecetini	Oecetis
Arthropoda	Insecta	Trichoptera	Leptoceridae	Leptocerinae	Triaenodini	Triaenodes
Arthropoda	Insecta	Trichoptera	Limnephilidae	Dicosmoecinae		Allocosmoecus
Arthropoda	Insecta	Trichoptera	Limnephilidae	Dicosmoecinae		Amphicosmoecus_canax
Arthropoda	Insecta	Trichoptera	Limnephilidae	Dicosmoecinae		Cryptochia
Arthropoda	Insecta	Trichoptera	Limnephilidae	Dicosmoecinae		Dicosmoecus
Arthropoda	Insecta	Trichoptera	Limnephilidae	Dicosmoecinae		Ecclisocosmoecus
Arthropoda	Insecta	Trichoptera	Limnephilidae	Dicosmoecinae		Ecclisomyia
Arthropoda	Insecta	Trichoptera	Limnephilidae	Dicosmoecinae		Onocosmoecus
Arthropoda	Insecta	Trichoptera	Limnephilidae	Limnephilinae	Chilostigmini	Desmona
Arthropoda	Insecta	Trichoptera	Limnephilidae	Limnephilinae	Chilostigmini	Glyphopsyche
Arthropoda	Insecta	Trichoptera	Limnephilidae	Limnephilinae	Chilostigmini	Homophylax
Arthropoda	Insecta	Trichoptera	Limnephilidae	Limnephilinae	Chilostigmini	Psychoglypha
Arthropoda	Insecta	Trichoptera	Limnephilidae	Limnephilinae	Limnephilini	Asynarchus
Arthropoda	Insecta	Trichoptera	Limnephilidae	Limnephilinae	Limnephilini	Grammotaulius

Phylum	Class	Order	Family	Subfamily	Tribe	OTU
Arthropoda	Insecta	Trichoptera	Limnephilidae	Limnephilinae	Limnephilini	Hesperophylax
Arthropoda	Insecta	Trichoptera	Limnephilidae	Limnephilinae	Limnephilini	Lenarchus
Arthropoda	Insecta	Trichoptera	Limnephilidae	Limnephilinae	Limnephilini	Limnephilus
Arthropoda	Insecta	Trichoptera	Limnephilidae	Limnephilinae	Stenophylacini	Chyrandra_centralis
Arthropoda	Insecta	Trichoptera	Limnephilidae	Limnephilinae	Stenophylacini	Clostoeca
Arthropoda	Insecta	Trichoptera	Limnephilidae	Limnephilinae	Stenophylacini	Hydatophylax
Arthropoda	Insecta	Trichoptera	Limnephilidae	Limnephilinae	Stenophylacini	Philocasca
Arthropoda	Insecta	Trichoptera	Limnephilidae	Pseudostenophylacinae		Pseudostenophylax
Arthropoda	Insecta	Trichoptera	Odontoceridae			Odontoceridae
Arthropoda	Insecta	Trichoptera	Philopotamidae	Chimarrinae		Chimarra
Arthropoda	Insecta	Trichoptera	Philopotamidae	Philopotaminae		Dolophilodes
Arthropoda	Insecta	Trichoptera	Philopotamidae	Philopotaminae		Wormaldia
Arthropoda	Insecta	Trichoptera	Phryganeidae			Phryganeidae
Arthropoda	Insecta	Trichoptera	Polycentropodidae			Polycentropodidae
Arthropoda	Insecta	Trichoptera	Psychomiidae	Psychomyiinae		Psychomyia
Arthropoda	Insecta	Trichoptera	Psychomiidae	Psychomyiinae		Tinodes
Arthropoda	Insecta	Trichoptera	Rhyacophilidae			Himalopsyche
Arthropoda	Insecta	Trichoptera	Rhyacophilidae			Rhyacophila
Arthropoda	Insecta	Trichoptera	Sericostomatidae	Sericostomatinae		Gumaga
Arthropoda	Insecta	Trichoptera	Uenoidae	Thremmatinae		Neophylax
Arthropoda	Insecta	Trichoptera	Uenoidae	Thremmatinae		Oligophlebodes
Arthropoda	Insecta	Trichoptera	Uenoidae	Uenoinae		Farula
Arthropoda	Insecta	Trichoptera	Uenoidae	Uenoinae		Neothremma
Arthropoda	Insecta	Trichoptera	Uenoidae	Uenoinae		Sericostriata
Arthropoda	Insecta	Tricladida	Planariidae			Turbellaria

Phylum	Class	Order	Family	Subfamily	Tribe	OTU
Coelenterata	Hydrazoa	Hydroida	Hydridae			Cnidaria
Mollusca	Bivalvia	Veneroida	Sphaeridae			Pisidiidae
Mollusca	Gastropoda	Basommatomorpha	Planorbidae			Planorbidae
Mollusca	Gastropoda	Basommatophora	Lymnaeidae			Lymnaeidae
Mollusca	Gastropoda	Basommatophora	Planorbidae			Planorbidae
Mollusca	Gastropoda	Limnophila	Ancylidae			Ferrissia
Mollusca	Gastropoda	Limnophila	Lymnaeidae			Lymnaeidae
Mollusca	Gastropoda	Limnophila	Physidae			Physa
Mollusca	Gastropoda	Limnophila	Planorbidae			Planorbidae
Mollusca	Gastropoda	Mesogastropoda	Hydrobiidae			Hydrobiidae
Mollusca	Gastropoda	Mesogastropoda	Hydrobiidae			Potamopyrgus_antipodarum
Mollusca	Gastropoda	Mesogastropoda	Pleuroceridae			Juga
Mollusca	Gastropoda	Neotaenioglossa	Hydrobiidae			Hydrobiidae
Mollusca	Pelecypoda		Margaritiferidae			Unionidae
Mollusca	Pelecypoda		Sphaeriidae			Pisidiidae
Mollusca	Pelecypoda		Unionidae			Unionidae
Mollusca	Pelecypoda	Unionoida	Margaritiferidae			Unionidae
Mollusca	Pelecypoda	Veneroida	Sphaeriidae			Pisidiidae
Nematoda						Nematoda
Nematomorpha						Nematomorpha
Nemertea						Prostoma
Platyhelminthes	Turbellaria					Turbellaria

Appendix B.

Table 7. Candidate predictor variables that were examined in PREDATOR model development.

Variable	Description	Transformation	Scale	Source
TEMPORAL				
Julian date	order number of the day starting from 1 January	none	Temporal	date of the macroinvertebrate sample
SPATIAL				
Longitude	longitudinal location of the site in decimal degrees	none	Point, bottom of reach	map
Latitude	latitudinal location of the site in decimal degrees	none	Point, bottom of reach	map
Elevation	elevation of the sampling site in meters determined by querying on 30 meter DEM	square-root	Point, bottom of reach	BLM/NED (http://www.or.blm.gov/gis/resources)
Eastern Oregon	East of Cascade crest (all Level III ecoregions east of the Cascades ecoregion)	Categorical - binary		http://www.epa.gov/wed/pages/ecoregions/na_eco.htm#Downloads
PHYSICAL/SIZE				
Stream Gradient (Map slope)	elevation change over the mapped sampling reach length divided by the reach length	square-root	Reach	1:24K USGS DRG Map
Drainage Area	area in hectares as defined by all water that flows through the sample point	Log10	Watershed upstream from bottom of reach	USU/DEQ
Stream Power	stream gradient multiplied by the square root of the drainage area	Log10	--	USU/DEQ
CLIMATE				
Annual Precipitation	mean annual precipitation at the sampling site in millimeters	none	Point	PRISM - NRCS Dr. Christopher Daly OSU (http://www.ncgc.nrcs.usda.gov/branch/gdb/products/climate/index.html)
Annual Maximum Temperature	mean annual maximum air temperature at sampling site in tenths of degrees Celsius	none	Point	PRISM - NRCS Dr. Christopher Daly OSU (http://www.ncgc.nrcs.usda.gov/branch/gdb/products/climate/index.html)
LEVEL 2 ECOREGION				
Marine Western Coastal Forest Ecoregion	level II ecoregion - Combined level III ecoregions 1 and 3	Categorical - binary	Point	http://www.epa.gov/wed/pages/ecoregions/na_eco.htm#Downloads
Western Cordillera Ecoregion	level II ecoregion - Combined level III ecoregions 4, 78, 11, and 9	Categorical - binary	Point	http://www.epa.gov/wed/pages/ecoregions/na_eco.htm#Downloads
Western Interior Basin and Range	level II ecoregion - Combined level III ecoregions 10, 12, and 80	Categorical - binary	Point	http://www.epa.gov/wed/pages/ecoregions/na_eco.htm#Downloads
LEVEL 3 ECOREGION				
Coast Range	Level III ecoregion 1	Categorical – binary	Point	http://www.epa.gov/wed/pages/ecoregions/na_eco.htm#Downloads
Willamette Valley	Level III ecoregion 3	Categorical – binary	Point	http://www.epa.gov/wed/pages/ecoregions/na_eco.htm#Downloads
Cascades	Level III ecoregion 4	Categorical – binary	Point	http://www.epa.gov/wed/pages/ecoregions/na_eco.htm#Downloads
Eastern Cascades Slopes and Foothills	Level III ecoregion 9	Categorical – binary	Point	http://www.epa.gov/wed/pages/ecoregions/na_eco.htm#Downloads
Columbia Plateau	Level III ecoregion 10	Categorical – binary	Point	http://www.epa.gov/wed/pages/ecoregions/na_eco.htm#Downloads
Blue Mountains	Level III ecoregion 11	Categorical – binary	Point	http://www.epa.gov/wed/pages/ecoregions/na_eco.htm#Downloads
Snake River	Level III ecoregion 12	Categorical –	Point	http://www.epa.gov/wed/pages/ecoregions/na_eco.htm#Downloads

Plains		binary		
Klamath Mountains	Level III ecoregion 78	Categorical – binary	Point	http://www.epa.gov/wed/pages/ecoregions/na_eco.htm#Downloads
Northern Basin and Range	Level III ecoregion 80	Categorical - binary	Point	http://www.epa.gov/wed/pages/ecoregions/na_eco.htm#Downloads
SOIL TYPE				
Erodible Lithology	Combined lithology types: alluvium, argillite and slate, conglomerate, dune sand, felsic pyroclastic, glacial drift, interlayered meta-sedimentary, lake sediment and playa, landslide, mafic pyroclastic, meta-sedimentary phylite and schist, mixed eugeosynchlinal, sandstone, shale and mudstone, siltstone, tuff	Categorical - binary	Point	Walker and MacLeod 1991 USGS
Resistant Lithology	Lithology types are combined into one of two classes: erodible or resistant	Categorical - binary	Point	Walker and MacLeod 1991 USGS

Appendix C.

Table 8. MWCF reference sites and corresponding environmental data. Level IV ecoregion: "1" = Coast Range, "3" = Willamette.

Level II ecoregion	Level IV ecoregion	Subbasin	Site name	Longitude	Latitude	Julian Date	Watershed Area (ha)	Elevation (m)	Map Slope (%)	Mean Annual Precipitation (mm)	Mean Annual Maximum Air Temperature (°C)
MWCF	1b	COOS	Dalton Cr.	-124.3252	43.2768	258	67	12	2.2	1643	166
MWCF	1b	COQUILLE	Bear Cr.	-124.2819	43.0206	265	283	137	2.6	1770	175
MWCF	1d	ALSEA	Cummins Cr.	-124.098	44.2669	218	2121	24	1.1	2014	160
MWCF	1d	ALSEA	Big Cr.	-124.1058	44.1707	207	3815	4	1.1	1944	160
MWCF	1d	ALSEA	Cummins Cr.	-124.091	44.2664	209	2076	19	1.2	2271	164
MWCF	1d	ALSEA	Rock Cr.	-124.0912	44.1877	208	1386	55	1.3	2189	163
MWCF	1d	ALSEA	Cummins Cr.	-124.0672	44.2686	188	1902	56	1.1	2284	163
MWCF	1d	NEHALEM	Harliss Cr.	-123.7186	45.6897	249	120	126	4.2	3571	148
MWCF	1d	NEHALEM	Trib to NF Wolf Cr.	-123.3837	45.7947	236	254	358	2.3	1958	142
MWCF	1d	SILETZ-YAQUINA	Boulder Cr.	-123.6283	44.9295	241	672	560	3.0	3762	112
MWCF	1d	WILSON-TRASK-NESTUCCA	Trib to Clear Cr.	-123.4881	45.4748	232	59	285	19.8	2515	132
MWCF	1d	WILSON-TRASK-NESTUCCA	Trib to Clear Cr.	-123.4877	45.4742	245	1660	269	2.2	2541	139
MWCF	1d	WILSON-TRASK-NESTUCCA	Company Cr.	-123.7435	45.5947	216	351	162	3.9	3594	152
MWCF	1f	LOWER COLUMBIA	Gnat Cr.	-123.4719	46.1123	252	870	565	4.8	2109	142
MWCF	1f	LOWER COLUMBIA	Elk Cr.	-123.5371	46.0577	266	1142	327	6.2	2973	142
MWCF	1f	NEHALEM	Trib to Gilmore Cr.	-123.5329	45.9601	176	79	233	7.0	2880	148
MWCF	1g	ALSEA	Flynn Cr.	-123.8533	44.5393	243	203	171	3.9	2262	167
MWCF	1g	ALSEA	Trout Cr.	-123.9527	44.4726	179	1604	36	2.6	2048	164
MWCF	1g	COQUILLE	Upper Rock Cr.	-123.7403	43.0903	195	55	809	8.4	2185	160
MWCF	1g	COQUILLE	Trib to WF Brummit Cr.	-123.8405	43.2112	219	37	668	8.1	2278	163
MWCF	1g	COQUILLE	Slater Cr.	-123.7995	42.9459	267	1554	213	2.9	1666	162
MWCF	1g	SILTCOOS	Fiddle Cr.	-123.9353	43.8856	187	822	92	1.3	2105	167
MWCF	1g	SIUSLAW	Green Leaf Cr.	-123.636	44.1602	184	75	256	1.9	2115	171
MWCF	1g	UMPQUA	MF NF Smith R.	-123.8208	43.8756	193	2429	112	1.4	1745	163
MWCF	1g	UMPQUA	Lost Cr.	-123.5218	43.4595	220	1805	89	1.1	1076	179
MWCF	1g	UMPQUA	Halfway Cr.	-123.5846	43.7485	221	202	189	3.0	1254	171
MWCF	1g	UMPQUA	Harvey Cr.	-123.941	43.7017	186	1954	42	0.4	1998	170
MWCF	1h	SIXES	NF Elk R.	-124.2018	42.7222	193	2301	333	1.6	2791	168
MWCF	3c	MOLALLA-PUDDING	Deer Cr.	-122.9209	45.0363	178	437	41	2.4	1047	174
MWCF	3c	UPPER WILLAMETTE	SF Berry Cr.	-123.2988	44.7076	187	407	124	2.8	1458	170

MWCF	3d	SOUTH SANTIAM	Trib to S Santiam R.	-122.8303	44.4138	214	308	211	14.5	1325	168
MWCF	3d	TUALATIN	Iler Cr.	-123.2686	45.5974	220	233	194	3.8	1673	150
MWCF	3d	TUALATIN	Roaring Cr.	-123.2537	45.5673	231	859	143	3.8	1608	153
MWCF	3d	TUALATIN	Bergholtzer Cr.	-123.2389	45.697	238	299	204	6.9	1776	154
MWCF	3d	TUALATIN	Scoggins Cr.	-123.2645	45.5154	246	3071	149	2.7	1631	150
MWCF	3d	TUALATIN	Beaver Cr.	-123.29	45.6676	248	2016	168	0.4	1475	149
MWCF	3d	UPPER WILLAMETTE	Jordan Cr.	-123.3006	43.932	224	240	158	1.5	1179	176
MWCF	3d	UPPER WILLAMETTE	Alder Cr.	-123.3491	44.5999	234	464	151	3.3	1621	166

Table 9. WC+CP reference sites and corresponding environmental data. Level IV ecoregion: "10" = Columbia Plateau, "11" = Blue Mountains, "4" = Cascades, "78" = Klamath Mountains, "9" = Eastern Cascades Slopes and Foothills.

Level II ecoregion	Level IV ecoregion	Subbasin	Site name	Longitude	Latitude	Julian Date	Area (ha)	Elevation (m)	Map Slope (%)	Mean Annual Precip. (mm)	Mean Annual Max. Air Temp.(°C)
NBR (Col. Plateau)	10a		California Cr.	-117.34700	47.51150	225	6939	588	4.8	1751	14.8
NBR (Col. Plateau)	10f		Cummings Cr.	-117.67200	46.32733	279	5185	643	3.4	1674	14.1
NBR (Col. Plateau)	10g		Umtanum Cr.	-120.57100	46.87700	265	998	605	4.2	1382	13.8
NBR (Col. Plateau)	10g		Quilomene Cr.	-120.09200	47.10240	183	5011	364	2.9	937	15.6
NBR (Col. Plateau)	10g		Oak Cr.	-120.87520	46.72900	224	7207	694	5.9	1534	13.1
NBR (Col. Plateau)	10g		Naneum Cr.	-120.47310	47.13830	225	1720	788	2.5	1724	11.8
WC	11a	LOWER JOHN DAY	Pine Cr.	-120.27586	44.90565	212	3866	754	2.9	381	15.8
WC	11a	UPPER JOHN DAY	Cottonwood Cr.	-119.63300	44.47800	228	7508	818	2.8	330	16.9
WC	11a	NORTH FORK JOHN DAY	Cabin Cr.	-119.36100	44.92500	247	1962	704	2.1	330	16.9
WC	11b	UPPER CROOKED	Allen Cr.	-120.17100	44.40200	235	1542	1478	2.4	584	12.1
WC	11c	UPPER GRANDE RONDE	Limber Jim Cr.	-118.29545	45.10703	271	94	1438	1.6	737	11.6
WC	11c	WALLA WALLA	Mill Cr.	-118.05983	45.98912	205	9194	735	1.1	1041	13.5
WC	11d	UPPER JOHN DAY	EF Canyon Cr.	-118.87895	44.26448	223	4123	1378	2.3	483	12.0
WC	11d	UPPER JOHN DAY	Reynolds Cr.	-118.51200	44.42149	212	2839	1338	3.1	635	13.4
WC	11d	UPPER JOHN DAY	Reynolds Cr.	-118.52200	44.42000	231	6035	1304	1.5	584	13.4
WC	11d	UPPER JOHN DAY	M. Fk. Canyon Cr.	-118.77542	44.25867	215	1184	1581	10.5	686	11.3
WC	11d	POWDER	Dutch Flat Cr.	-118.12600	44.95900	229	2338	1596	0.4	686	11.7
WC	11e	WALLOWA	Minam R.	-117.67563	45.40631	257	44647	1035	1.1	889	10.5
WC	11e	WALLOWA	Little Minam R.	-117.67200	45.38400	230	11240	1087	1.8	838	9.7
WC	11e	POWDER	Eagle Cr.	-117.44000	45.04100	242	5896	1451	0.4	1092	10.0
WC	11f	LOWER GRANDE RONDE	Wenaha R.	-117.60066	45.97762	256	49435	646	1.3	635	13.1
WC	11h	UPPER MALHEUR	Little Malheur R.	-118.31100	44.25000	233	5358	1566	1.3	737	11.8
WC	11h	UPPER	Little	-118.31527	44.25178	217	4246	1573	13.0	737	11.8

		MALHEUR	Malheur R.								
WC	11l	NORTH FORK JOHN DAY	Onion Cr.	-118.38236	44.89782	212	608	1693	3.2	787	11.3
WC	11l	NORTH FORK JOHN DAY	Baldy Cr.	-118.31402	44.90789	211	2531	1700	3.4	838	10.8
WC	11l	NORTH FORK JOHN DAY	Martin Cr.	-118.54964	44.95504	197	586	1674	3.1	787	11.3
WC	11l	NORTH FORK JOHN DAY	NF Cable Cr.	-118.66512	45.05127	198	719	1420	2.1	737	11.6
WC	11l	MIDDLE FORK JOHN DAY	Big Cr.	-118.68610	44.77780	205	296	1867	4.2	838	10.6
WC	11l	NORTH FORK JOHN DAY	Big Cr.	-118.60358	45.01550	204	1088	1554	1.9	787	11.7
WC	11l	MIDDLE FORK JOHN DAY	Upper Big Cr.	-118.69614	44.78433	204	491	1831	1.8	838	11.0
WC	11l	NORTH FORK JOHN DAY	SF Desolation Cr.	-118.67306	44.79158	238	2358	1682	6.8	838	10.6
WC	11l	NORTH FORK JOHN DAY	S.F. Desolation Cr.	-118.68400	44.81400	248	2837	1607	1.9	787	10.6
WC	11l	NORTH FORK JOHN DAY	Baldy Cr.	-118.30700	44.90000	228	2420	1749	1.9	838	10.8
WC	11l	UPPER GRANDE RONDE	Beaver Cr.	-118.20870	45.14693	222	3996	1497	5.3	787	11.6
WC	11l	UPPER GRANDE RONDE	Limber Jim Cr.	-118.53180	45.09080	199	2106	1456	2.5	737	11.8
WC	11l	WALLOWA	W.F. Wallowa R.	-117.23500	45.22000	226	5090	1791	0.3	1600	7.8
WC	11l	UPPER GRANDE RONDE	N. Fk. Catherine Cr.	-117.61222	45.15672	210	3826	1314	10.2	1041	9.4
WC	11l	IMNAHA	Imnaha R.	-117.02100	45.11043	211	17208	1390	0.1	1295	10.5
WC	11l	POWDER	Rock Cr.	-118.10343	44.88639	230	4824	1604	3.3	737	12.4
WC	11m	UPPER JOHN DAY	Strawberry Cr.	-118.69714	44.29466	210	259	2104	10.9	1143	11.8
WC	11m	UPPER JOHN DAY	Strawberry Cr.	-118.69052	44.30075	211	366	1970	8.2	1092	11.8
WC	11m	WALLOWA	N Minam R.	-117.46621	45.27151	253	3162	1644	0.8	1549	8.4
WC	11m	WALLOWA	E.F. Lostine R.	-117.34800	45.21600	229	988	2156	0.5	1702	7.5
WC	11m	IMNAHA	McCully Cr.	-117.15300	45.21500	228	255	2370	1.7	1702	8.0
WC	11m	POWDER	EF Eagle Cr.	-117.31893	45.15849	256	144	2118	19.1	1753	7.7
WC	4a	LOWER COLUMBIA-SANDY	Lady Cr.	-121.83532	45.31646	241	1000	778	3.1	2311	11.1
WC	4a	LOWER COLUMBIA-SANDY	Lost Cr.	-121.84825	45.38499	238	2011	682	4.0	2667	11.6
WC	4a	LOWER COLUMBIA-SANDY	Tanner Cr.	-121.95207	45.62197	245	6877	57	9.0	1905	14.7
WC	4a	LOWER COLUMBIA-SANDY	Cast Cr.	-121.85295	45.37583	215	464	708	9.4	2515	12.2
WC	4a	LOWER COLUMBIA-SANDY	Bull Run R.	-121.88868	45.48103	250	1885	742	6.6	2870	11.6
WC	4a	LOWER COLUMBIA-SANDY	SF Salmon R.	-121.93954	45.26962	225	3072	507	3.5	2057	13.2
WC	4a	LOWER COLUMBIA-SANDY	Salmon R.	-121.93750	45.27337	225	21413	535	1.5	2057	13.2

WC	4a	LOWER COLUMBIA-SANDY	Fir Cr.	-122.02499	45.48101	230	1431	486	5.6	2261	14.5
WC	4a	MIDDLE COLUMBIA-HOOD	Herman Cr.	-121.83534	45.67853	196	9126	172	5.0	2362	15.6
WC	4a	MIDDLE COLUMBIA-HOOD	Harphon Cr.	-121.76515	45.68725	197	275	104	17.4	1803	15.3
WC	4a	MIDDLE COLUMBIA-HOOD	Eagle Cr.	-121.86972	45.59537	251	5358	251	2.9	2362	12.9
WC	4a	NORTH UMPQUA	East Copeland Cr.	-122.52135	43.23377	233	928	732	4.3	1295	14.5
WC	4a	NORTH UMPQUA	Canton Cr.	-122.72469	43.49055	252	1127	660	3.2	1651	15.7
WC	4a	NORTH UMPQUA	Canton Cr.	-122.72615	43.48689	210	1690	649	1.3	1651	15.8
WC	4a	MCKENZIE	French Pete Cr.	-122.19510	44.04191	235	8030	603	6.8	1803	14.8
WC	4a	CLACKAMAS	Dickey Cr.	-122.05389	44.93045	234	1976	762	5.9	2108	12.7
WC	4a	MIDDLE FORK WILLAMETTE	Trib to Goodman Cr.	-122.67695	43.82910	236	504	393	12.2	1448	16.2
WC	4a	MIDDLE FORK WILLAMETTE	NF MF Willamette R.	-122.28875	43.88823	241	34352	638	0.7	1702	14.5
WC	4a	NORTH SANTIAM	Rock Cr.	-122.39721	44.69876	243	2375	579	2.9	2210	14.2
WC	4a	MCKENZIE	Lookout Cr.	-122.15895	44.23210	195	1565	725	5.3	2311	14.0
WC	4a	COAST FORK WILLAMETTE	Trib to Bear Cr.	-122.94898	43.89032	225	419	270	5.2	1346	17.0
WC	4a	MCKENZIE	Marten Cr.	-122.52517	44.12009	227	2585	268	2.2	1448	16.8
WC	4a	MCKENZIE	Cash Cr.	-122.88053	44.23008	233	920	382	7.2	1499	16.2
WC	4a	MCKENZIE	SF McKenzie R.	-122.05685	43.95979	246	13182	830	1.6	1753	12.9
WC	4a	MCKENZIE	Trib to SF McKenzie	-122.11595	43.95167	248	263	861	23.1	1803	13.4
WC	4a	MOLALLA-PUDDING	Trout Cr.	-122.44564	45.04075	273	2471	449	3.7	2007	14.8
WC	4a	SOUTH SANTIAM	Moose Cr.	-122.38619	44.42754	222	3600	389	2.6	1702	15.5
WC	4a	CLACKAMAS	Delph Cr.	-122.24392	45.26692	223	1669	328	0.6	1549	16.2
WC	4a	MIDDLE FORK WILLAMETTE	Shortridge Cr.	-122.48579	43.73887	194	519	348	7.9	1245	16.0
WC	4a	SOUTH SANTIAM	Donaca Cr.	-122.19130	44.51892	208	276	615	15.8	2261	13.0
WC	4a	SOUTH SANTIAM	Donaca Cr.	-122.19020	44.51914	224	290	625	14.2	2261	13.1
WC	4a	CLACKAMAS	Upper Hot Springs Cr.	-122.16938	44.95037	224	3999	643	1.7	2210	12.0
WC	4a	MCKENZIE	King Cr.	-122.16800	44.16170	220	38937	435	6.2	1448	15.8
WC	4a	MIDDLE FORK WILLAMETTE	Bedrock Cr.	-122.54414	43.97354	219	354	342	3.6	1549	16.0
WC	4a	MCKENZIE	Tipsoo Cr.	-122.20697	44.04921	220	195	771	10.5	1803	14.8
WC	4a	MCKENZIE	French Pete Cr.	-122.20323	44.04291	220	8110	568	4.6	1803	14.8
WC	4a	SOUTH SANTIAM	Keith Cr.	-122.28402	44.40748	228	471	467	13.1	2007	13.8
WC	4a	SOUTH SANTIAM	Trout Cr.	-122.34636	44.39880	228	975	389	3.9	2007	15.1
WC	4a	CLACKAMAS	Roaring Cr.	-122.11186	45.16138	231	10603	334	5.7	1803	14.7
WC	4a	CLACKAMAS	Eagle Cr.	-122.10135	45.29933	229	3734	494	3.0	2210	13.3
WC	4a	MCKENZIE	King Cr.	-122.17071	44.15300	220	1186	593	6.6	1600	15.8
WC	4a	SOUTH SANTIAM	Egg Cr.	-122.21295	44.51842	223	163	589	32.9	2311	13.0

WC	4a	COAST FORK WILLAMETTE	Cedar Cr.	-122.72368	43.54734	210	600	679	9.3	1702	15.1
WC	4a	COAST FORK WILLAMETTE	Martin Cr.	-122.71896	43.54496	210	234	754	9.9	1702	15.1
WC	4a	CLACKAMAS	Dickey Cr.	-122.05412	44.92941	224	1969	771	5.3	2108	12.7
WC	4a	MIDDLE FORK WILLAMETTE	Logan Cr.	-122.47800	43.95680	219	1400	435	9.7	1600	15.5
WC	4b	LOWER COLUMBIA-SANDY	Tumbling Cr.	-121.88150	45.23283	251	1218	715	8.1	1956	11.5
WC	4b	LOWER COLUMBIA-SANDY	Bighorn Cr.	-121.92068	45.26190	217	240	534	13.7	2007	12.5
WC	4b	MIDDLE COLUMBIA-HOOD	Lake Branch Cr.	-121.84321	45.51650	194	1746	699	2.4	2870	11.8
WC	4b	MIDDLE COLUMBIA-HOOD	McGee Cr.	-121.77351	45.43014	229	975	860	2.5	2718	9.2
WC	4b	NORTH UMPQUA	Fish Cr.	-122.40954	43.09827	225	338	1513	1.1	1448	11.4
WC	4b	NORTH UMPQUA	Boulder Cr.	-122.50880	43.33037	244	6109	703	2.5	1245	15.4
WC	4b	MIDDLE FORK WILLAMETTE	Black Cr.	-122.17709	43.71478	243	5188	918	0.3	1651	13.8
WC	4b	MIDDLE FORK WILLAMETTE	Fisher Cr.	-122.13559	43.86306	241	2839	823	5.2	1651	13.7
WC	4b	NORTH SANTIAM	Opal Cr.	-122.20803	44.84536	242	2728	632	2.1	2464	12.8
WC	4b	NORTH SANTIAM	SF Breitenbush R.	-121.93993	44.76983	243	4998	756	3.6	1854	13.4
WC	4b	MCKENZIE	Trib to Rebel Cr.	-122.14610	44.02313	194	52	958	29.1	1854	14.3
WC	4b	NORTH SANTIAM	Tincup Cr.	-122.28132	44.86329	213	83	736	21.4	2464	13.0
WC	4b	MIDDLE FORK WILLAMETTE	Eagle Cr.	-122.19464	43.68558	218	1817	1135	4.3	1651	14.1
WC	4b	MCKENZIE	SF McKenzie R.	-121.98620	43.95494	247	6480	959	2.1	1803	12.5
WC	4b	CLACKAMAS	Doris Cr.	-122.16762	44.91611	230	67	784	21.9	2311	12.3
WC	4b	CLACKAMAS	Hot Springs Fork Collawash R.	-122.14237	44.88839	232	648	920	3.6	2565	12.3
WC	4b	NORTH SANTIAM	Little North Santaim R.	-122.29003	44.85315	246	8317	475	1.6	2413	13.0
WC	4b	CLACKAMAS	Roaring R.	-121.93803	45.19645	267	1405	923	4.2	2057	11.3
WC	4b	CLACKAMAS	Welcome Cr.	-122.04160	44.87840	272	424	849	9.7	1956	12.2
WC	4b	CLACKAMAS	Elk Lake Cr.	-122.00845	44.88987	190	6895	719	1.9	1905	12.2
WC	4b	MCKENZIE	Roney Cr.	-122.01967	44.10760	202	476	676	15.0	1905	13.9
WC	4b	MIDDLE FORK WILLAMETTE	Black Cr.	-122.10088	43.70004	229	1543	1079	13.1	1702	11.4
WC	4b	CLACKAMAS	Battle Cr.	-122.07300	44.84753	243	1536	866	3.9	2108	12.9
WC	4b	NORTH SANTIAM	Crag Cr.	-121.88874	44.73813	265	282	933	9.9	2007	13.2
WC	4b	MIDDLE FORK WILLAMETTE	Fisher Cr.	-122.12762	43.85665	219	2545	868	3.3	1651	13.7
WC	4b	MCKENZIE	Eugene Cr.	-122.00891	44.05882	220	5303	840	4.9	1905	13.1
WC	4b	MCKENZIE	Separation Cr.	-122.00392	44.12679	223	14194	698	4.2	1854	14.8
WC	4b	MIDDLE	NF MF	-122.07191	43.87530	221	18753	894	2.4	1702	12.7

		FORK WILLAMETTE	Willamtte R.								
WC	4b	NORTH SANTIAM	Opal Cr.	-122.20207	44.84289	229	2512	696	5.1	2464	12.8
WC	4b	NORTH SANTIAM	Battle Axe Cr.	-122.16729	44.85558	229	1032	802	3.1	2667	12.4
WC	4b	MCKENZIE	Roney Cr.	-122.01753	44.10788	220	438	702	4.2	1905	13.9
WC	4b	MCKENZIE	Horse Cr.	-122.01840	44.07177	221	13750	792	2.5	1905	13.1
WC	4b	NORTH SANTIAM	Cheat Cr.	-121.92055	44.70736	223	454	1023	15.5	2007	13.2
WC	4b	NORTH SANTIAM	SF Breitenbush R.	-121.88554	44.73921	223	2148	925	3.9	2007	13.2
WC	4c	LOWER DESCHUTES	Mill Cr.	-121.75178	44.79520	257	2054	1421	1.3	2210	11.2
WC	4c	LOWER COLUMBIA-SANDY	Rushing Water Cr.	-121.77785	45.37188	217	241	1058	9.8	2565	7.7
WC	4c	MIDDLE COLUMBIA-HOOD	Cold Spring Cr.	-121.60804	45.35520	250	453	1479	4.5	2210	8.6
WC	4c	MIDDLE COLUMBIA-HOOD	Cold Springs Cr.	-121.59067	45.39689	271	1961	1107	4.7	2159	10.0
WC	4c	MIDDLE FORK WILLAMETTE	Bear Cr.	-122.20504	43.55441	234	914	1382	15.9	1651	13.1
WC	4c	NORTH SANTIAM	Trib to Marion Cr.	-121.93481	44.59246	211	503	806	1.7	1854	13.5
WC	4c	MIDDLE FORK WILLAMETTE	Shady Cr.	-122.18884	43.61984	238	73	1448	30.9	1600	13.7
WC	4c	MIDDLE FORK WILLAMETTE	Gold Lake Cr.	-122.03097	43.64372	245	3664	1466	0.3	1753	11.2
WC	4c	CLACKAMAS	Slow Cr.	-121.77675	44.90098	224	376	1304	1.2	1905	10.4
WC	4c	NORTH SANTIAM	NF Santiam R.	-121.92270	44.49514	223	2024	1360	5.0	2057	11.6
WC	4d	MIDDLE COLUMBIA-HOOD	Trib to Polallie Cr.	-121.63345	45.38656	226	228	1702	18.1	3175	10.0
WC	4e	UPPER KLAMATH LAKE	Rock Cr.	-122.12968	42.56007	185	2438	1487	1.8	1346	12.5
WC	4e	NORTH UMPQUA	Lake Cr.	-122.17159	43.25243	224	15483	1376	1.6	1194	13.2
WC	4e	NORTH UMPQUA	Clearwater R.	-122.22998	43.24455	201	1303	1264	2.6	1194	13.3
WC	4f	UPPER ROGUE	SF Rogue R.	-122.27775	42.55974	209	4120	1432	2.6	1346	11.9
WC	4f	SOUTH UMPQUA	Castle Rock Cr.	-122.51800	43.11322	210	4437	835	8.1	1295	14.0
WC	4f	SOUTH UMPQUA	Fish Lake Cr.	-122.55415	43.08846	210	2809	753	1.9	1245	14.0
WC	4f	SOUTH UMPQUA	Squaw Cr.	-122.65500	42.94500	209	2761	732	5.0	1194	13.0
WC	4f	SOUTH UMPQUA	Donegan Cr.	-122.65566	42.94481	209	1763	710	3.6	1194	13.0
WC	4f	UPPER ROGUE	Upper Bitterlick Cr.	-122.64662	42.82720	203	3140	747	2.9	1194	13.4
WC	4f	UPPER ROGUE	Big Ben Cr.	-122.31623	42.63752	209	2645	1253	10.5	1194	12.8
WC	78d	CHETCO	Chetco R.	-123.91227	42.17385	256	2627	625	3.0	3429	16.6
WC	78e	APPLEGATE	Osier Cr.	-123.24006	42.07481	200	83	1111	33.8	1295	13.1
WC	78e	LOWER ROGUE	Rueben Cr.	-123.57204	42.65526	206	2527	236	4.6	1041	15.6
WC	78e	LOWER ROGUE	Whisky Cr.	-123.63248	42.66427	269	3786	242	6.3	1041	15.8
WC	78e	MIDDLE ROGUE	WF Ashland Cr.	-122.71851	42.14356	201	2556	969	6.5	838	13.3

WC	78e	MIDDLE ROGUE	WF Ashland Cr.	-122.71527	42.14609	208	129	970	5.1	838	13.3
WC	78f	SMITH CAL OR	NF Smith R.	-123.98200	42.04240	184	9158	433	1.8	2565	16.4
WC	78f	SMITH CAL OR	Left Fork Chrome Cr.	-123.97130	42.05301	185	3876	416	4.2	2718	16.7
WC	78f	CHETCO.CALIFORNIA OREGON	EF Winchuck R.	-124.09119	42.05009	236	3344	78	0.9	2261	16.3
WC	78f	LOWER ROGUE	Shasta Costa Cr.	-124.03501	42.57303	238	8800	52	0.6	1905	20.1
WC	9b	LOWER DESCHUTES	Little Badger Cr.	-121.44904	45.30092	192	190	1222	8.7	940	12.0
WC	9b	LOWER DESCHUTES	Tygh Cr.	-121.37563	45.31173	226	1368	794	10.4	584	13.9
WC	9b	MIDDLE COLUMBIA-HOOD	SF Mill Cr.	-121.45411	45.47498	195	1468	766	3.4	1245	12.8
WC	9b	MIDDLE COLUMBIA-HOOD	SF Mill Cr.	-121.44268	45.47860	196	3611	734	3.6	1143	12.8
WC	9d	LOWER DESCHUTES	Shitike Cr.	-121.65073	44.74714	256	5373	1105	0.7	1143	12.3
WC	9d	UPPER DESCHUTES	Candle Cr.	-121.68267	44.58685	224	1168	957	0.5	737	13.0
WC	9e	WILLIAMSON	Miller Cr.	-121.93698	43.21295	184	3284	1693	0.9	991	12.0
WC	9e	SUMMER LAKE	WF Silver Cr.	-121.25880	42.94294	228	630	1914	3.5	1041	11.5
WC	9e	SUMMER LAKE	Buck Cr.	-121.29843	43.00178	186	2340	1784	2.0	991	11.7
WC	9f	LITTLE DESCHUTES	Paulina Cr.	-121.42500	43.72500	175	5992	1309	0.7	483	13.3
WC	9h	LAKE ABERT	Dairy Cr.	-120.75070	42.48855	188	3985	1779	1.2	737	12.3